

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Choi et. al.

(ii) TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

(iii) NUMBER OF SEQUENCES: 452

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Human Genome Sciences, Inc.
- (B) STREET: 9410 Key West Avenue
- (C) CITY: Rockville
- (D) STATE: Maryland
- (E) COUNTRY: USA
- (F) ZIP: 20850

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
- (B) COMPUTER: HP Vectra 486/33
- (C) OPERATING SYSTEM: MSDOS version 6.2
- (D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: Unassigned
- (B) FILING DATE: Herewith
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/961,083
- (B) FILING DATE: OCT-30-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Michelle S. Marks
- (B) REGISTRATION NUMBER: 41,971
- (C) REFERENCE/DOCKET NUMBER: PB340P2C1

(vi) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (301) 309-8504
- (B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TAAAATCTAC	GACAATAAAA	ATCAACTCAT	TGCTGACTTG	GGTTCTGAAC	GCCGCGTCAA	60
TGCCCCAAGCT	AATGATATTC	CCACAGATTT	GGTTAAGGCA	ATCGTTTCTA	TCGAAGACCA	120
TCGCTTCTTC	GACCACAGGG	GGATTGATAC	CATCCGTATC	CTGGGAGCTT	TCTTGCGCAA	180
TCTGCAAAGC	AATTCCTCC	AAGGTGGATC	AACTCTCACC	CAACAGTTGA	TTAAGTTGAC	240
TTACTTTTCA	ACTTCGACTT	CCGACCAGAC	TATTTCTCGT	AAGGCTCAGG	AAGCTTGGTT	300
AGCGATTTCAG	TTAGAACAAA	AAGCAACCAA	GCAAGAAATC	TTGACCTACT	ATATAAATAA	360
GGTCTACATG	TCTAATGGGA	ACTATGGAAT	GCAGACAGCA	GCTCAAAACT	ACTATGGTAA	420
AGACCTCAAT	AATTTAAGTT	TACCTCAGTT	AGCCTTGCTG	GCTGGAATGC	CTCAGGCACC	480
AAACCAATAT	GACCCCTATT	CACATCCAGA	AGCAGCCCAA	GACCGCCGAA	ACTTGGTCTT	540
ATCTGAAATG	AAAAATCAAG	GCTACATCTC	TGCTGAACAG	TATGAGAAAG	CAGTCAATAC	600
ACCAATTACT	GATGGACTAC	AAAGTCTCAA	ATCAGCAAGT	AATTACCCTG	CTTACATGGA	660
TAATTACCTC	AAGGAAGTCA	TCAATCAAGT	TGAAGAAGAA	ACAGGCTATA	ACCTACTCAC	720
AACTGGGATG	GATGTCTACA	CAAATGTAGA	CCAAGAAGCT	CAAAAACATC	TGTGGGATAT	780
TTACAATACA	GACGAATACG	TTGCCTATCC	AGACGATGAA	TTGCAAGTCG	CTTCTACCAT	840
TGTTGATGTT	TCTAACGGTA	AAGTCATTGC	CCAGCTAGGA	GCACGCCATC	AGTCAAGTAA	900
TGTTTCCTTC	GGAATTAACC	AAGCAGTAGA	AACAAACCGC	GA CTGGGGAT	CAACTATGAA	960
ACCGATCACA	GACTATGCTC	CTGCCTTGGA	GTACGGTGTC	TACGATTCAA	CTGCTACTAT	1020
CGTTCACGAT	GAGCCCTATA	ACTACCCTGG	GACAAATACT	CCTGTTTATA	ACTGGGATAG	1080
GGGCTACTTT	GGCAACATCA	CCTTGCAATA	CGCCCTGCAA	CAATCGCGAA	ACGTCCCAGC	1140
CGTGGAAACT	CTAAACAAGG	TCGGACTCAA	CCGCGCCAAG	ACTTTCCTAA	ATGGTCTAGG	1200
AATCGACTAC	CCAAGTATTC	ACTACTCAAA	TGCCATTTCA	AGTAACACAA	CCGAATCAGA	1260
CAAAAAATAT	GGAGCAAGTA	GTGAAAAGAT	GGCTGCTGCT	TACGCTGCCT	TTGCAAATGG	1320
TGGAACTTAC	TATAAACCAA	TGTATATCCA	TAAAGTCGTC	TTTAGTGATG	GGAGTGAAAA	1380
AGAGTTCTCT	AATGTCGGAA	CTCGTGCCAT	GAAGGAAACG	ACAGCCTATA	TGATGACCGA	1440
CATGATGAAA	ACAGTCTTGA	CTTATGGAAC	TGGACGAAAT	GCCTATCTTG	CTTGGCTCCC	1500
TCAGGCTGGT	AAAACAGGAA	CCTCTAACTA	TACAGACGAG	GAAATTGAAA	ACCACATCAA	1560
GACCTCTCAA	TTTGTAGCAC	CTGATGAACT	ATTTGCTGGC	TATACGCGTA	AATATTCAAT	1620
GGCTGTATGG	ACAGGCTATT	CTAACCGTCT	GACACCACTT	G TAGGCAATG	GCCTTACGGT	1680
CGCTGCCAAA	GTTTACCGCT	CTATGATGAC	CTACCTGTCT	GAAGGAAGCA	ATCCAGAAGA	1740

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TTGGAATATA CCAGAGGGGC TCTACAGAAA TGGAGAATTC GTATTTAAAA ATGGTGCTCG      1800
TTCTACGTGG AACTCACCTG CTCCACAACA ACCCCCATCA ACTGAAAGTT CAAGCTCATC      1860
ATCAGATAGT TCAACTTCAC AGTCTAGCTC AACCACTCCA AGCACAAATA ATAGTACGAC      1920
TACCAATCCT AACAAATAATA CGCAACAATC AAATACAACC CCTGATCAAC AAAATCAGAA      1980
TCCTCAACCA GCACAACCA                                     1999

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala Asp Leu Gly Ser Glu
1           5           10           15
Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro Thr Asp Leu Val Lys
          20           25           30
Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe Asp His Arg Gly Ile
          35           40           45
Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg Asn Leu Gln Ser Asn
          50           55           60
Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Leu Thr
          65           70           75           80
Tyr Phe Ser Thr Ser Thr Ser Asp Gln Thr Ile Ser Arg Lys Ala Gln
          85           90           95
Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys Ala Thr Lys Gln Glu
          100          105          110
Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met Ser Asn Gly Asn Tyr
          115          120          125
Gly Met Gln Thr Ala Ala Gln Asn Tyr Tyr Gly Lys Asp Leu Asn Asn
          130          135          140
Leu Ser Leu Pro Gln Leu Ala Leu Leu Ala Gly Met Pro Gln Ala Pro
          145          150          155          160
Asn Gln Tyr Asp Pro Tyr Ser His Pro Glu Ala Ala Gln Asp Arg Arg
          165          170          175
Asn Leu Val Leu Ser Glu Met Lys Asn Gln Gly Tyr Ile Ser Ala Glu
          180          185          190
Gln Tyr Glu Lys Ala Val Asn Thr Pro Ile Thr Asp Gly Leu Gln Ser
          195          200          205
Leu Lys Ser Ala Ser Asn Tyr Pro Ala Tyr Met Asp Asn Tyr Leu Lys

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210				215				220							
Glu 225	Val	Ile	Asn	Gln 230	Val	Glu	Glu	Glu	Thr	Gly 235	Tyr	Asn	Leu	Leu	Thr 240
Thr	Gly	Met	Asp	Val 245	Tyr	Thr	Asn	Val	Asp 250	Gln	Glu	Ala	Gln	Lys 255	His
Leu	Trp	Asp	Ile 260	Tyr	Asn	Thr	Asp	Glu 265	Tyr	Val	Ala	Tyr	Pro 270	Asp	Asp
Glu	Leu	Gln 275	Val	Ala	Ser	Thr	Ile 280	Val	Asp	Val	Ser	Asn 285	Gly	Lys	Val
Ile	Ala 290	Gln	Leu	Gly	Ala	Arg 295	His	Gln	Ser	Ser	Asn 300	Val	Ser	Phe	Gly
Ile 305	Asn	Gln	Ala	Val	Glu 310	Thr	Asn	Arg	Asp	Trp 315	Gly	Ser	Thr	Met	Lys 320
Pro	Ile	Thr	Asp	Tyr 325	Ala	Pro	Ala	Leu	Glu 330	Tyr	Gly	Val	Tyr	Asp 335	Ser
Thr	Ala	Thr	Ile 340	Val	His	Asp	Glu	Pro 345	Tyr	Asn	Tyr	Pro	Gly 350	Thr	Asn
Thr	Pro	Val 355	Tyr	Asn	Trp	Asp	Arg 360	Gly	Tyr	Phe	Gly	Asn 365	Ile	Thr	Leu
Gln	Tyr 370	Ala	Leu	Gln	Gln	Ser 375	Arg	Asn	Val	Pro	Ala 380	Val	Glu	Thr	Leu
Asn 385	Lys	Val	Gly	Leu	Asn 390	Arg	Ala	Lys	Thr	Phe 395	Leu	Asn	Gly	Leu	Gly 400
Ile	Asp	Tyr	Pro	Ser 405	Ile	His	Tyr	Ser	Asn 410	Ala	Ile	Ser	Ser	Asn 415	Thr
Thr	Glu	Ser	Asp 420	Lys	Lys	Tyr	Gly	Ala 425	Ser	Ser	Glu	Lys	Met 430	Ala	Ala
Ala	Tyr	Ala 435	Ala	Phe	Ala	Asn	Gly 440	Gly	Thr	Tyr	Tyr	Lys 445	Pro	Met	Tyr
Ile	His 450	Lys	Val	Val	Phe	Ser 455	Asp	Gly	Ser	Glu	Lys 460	Glu	Phe	Ser	Asn
Val 465	Gly	Thr	Arg	Ala	Met 470	Lys	Glu	Thr	Thr	Ala 475	Tyr	Met	Met	Thr	Asp 480
Met	Met	Lys	Thr	Val 485	Leu	Thr	Tyr	Gly	Thr 490	Gly	Arg	Asn	Ala	Tyr 495	Leu
Ala	Trp	Leu	Pro 500	Gln	Ala	Gly	Lys	Thr 505	Gly	Thr	Ser	Asn	Tyr 510	Thr	Asp
Glu	Glu	Ile 515	Glu	Asn	His	Ile	Lys 520	Thr	Ser	Gln	Phe	Val 525	Ala	Pro	Asp
Glu	Leu 530	Phe	Ala	Gly	Tyr	Thr 535	Arg	Lys	Tyr	Ser	Met 540	Ala	Val	Trp	Thr
Gly	Tyr	Ser	Asn	Arg	Leu	Thr	Pro	Leu	Val	Gly	Asn	Gly	Leu	Thr	Val

545		550		555		560									
Ala	Ala	Lys	Val	Tyr	Arg	Ser	Met	Met	Thr	Tyr	Leu	Ser	Glu	Gly	Ser
				565					570					575	
Asn	Pro	Glu	Asp	Trp	Asn	Ile	Pro	Glu	Gly	Leu	Tyr	Arg	Asn	Gly	Glu
			580					585					590		
Phe	Val	Phe	Lys	Asn	Gly	Ala	Arg	Ser	Thr	Trp	Asn	Ser	Pro	Ala	Pro
			595				600					605			
Gln	Gln	Pro	Pro	Ser	Thr	Glu	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Ser
	610					615						620			
Thr	Ser	Gln	Ser	Ser	Ser	Thr	Thr	Pro	Ser	Thr	Asn	Asn	Ser	Thr	Thr
	625					630				635					640
Thr	Asn	Pro	Asn	Asn	Asn	Thr	Gln	Gln	Ser	Asn	Thr	Thr	Pro	Asp	Gln
			645						650					655	
Gln	Asn	Gln	Asn	Pro	Gln	Pro	Ala	Gln	Pro						
			660					665							

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAATTACAAT ACGGACTATG AATTGACCTC TGGAGAAAAA TTACCTCTTC CTAAAGAGAT	60
TTCAGGTTAC ACTTATATTG GATATATCAA AGAGGGAAAA ACGACTTCTG AGTCTGAAGT	120
AAGTAATCAA AAGAGTTCAG TTGCCACTCC TACAAAACAA CAAAAGGTGG ATTATAATGT	180
TACACCGAAT TTTGTAGACC ATCCATCAAC AGTACAAGCT ATTCAGGAAC AAACACCTGT	240
TTCTTCAACT AAGCCGACAG AAGTTCAAGT AGTTGAAAAA CCTTTCTCTA CTGAATTAAT	300
CAATCCAAGA AAAGAAGAGA AACAATCTTC AGATTCTCAA GAACAATTAG CCGAACATAA	360
GAATCTAGAA ACGAAGAAAG AGGAGAAGAT TTCTCCAAAA GAAAAGACTG GGGTAAATAC	420
ATTAAATCCA CAGGATGAAG TTTTATCAGG TCAATTGAAC AAACCTGAAC TCTTATATCG	480
TGAGGAAACT ATGGAGACAA AAATAGATTT TCAAGAAGAA ATTCAAGAAA ATCCTGATTT	540
AGCTGAAGGA ACTGTAAGAG TAAAACAAGA AGGTAAATTA GGTAAGAAAG TTGAAATCGT	600
CAGAATATTC TCTGTAAACA AGGAAGAAGT TTCGCGAGAA ATTGTTTCAA CTTCAACGAC	660
TGCGCCTAGT CCAAGAATAG TCGAAAAAGG TACTAAAAAA ACTCAAGTTA TAAAGGAACA	720
ACCTGAGACT GGTGTAGAAC ATAAGGACGT ACAGTCTGGA GCTATTGTTG AACCCGCAAT	780
TCAGCCTGAG TTGCCCCAAG CTGTAGTAAG TGACAAAGGC GAACCAGAAG TTCAACCTAC	840

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ATTACCCGAA GCAGTTGTGA CCGACAAAGG TGAGACTGAG GTTCAACCAG AGTCGCCAGA      900
TACTGTGGTA AGTGATAAAG GTGAACCAGA GCAGGTAGCA CCGCTTCCAG AATATAAGGG      960
TAATATTGAG CAAGTAAAC CTGAAACTCC GGTTGAGAAG ACCAAAGAAC AAGGTCCAGA      1020
AAAAACTGAA GAAGTTCCAG TAAACCAAC AGAAGAAACA CCAGTAAATC CAAATGAAGG      1080
TACTACAGAA GGAACCTCAA TTCAAGAAGC AGAAAATCCA GTTCAACCTG CAGAAGAATC      1140
AACAACGAAT TCAGAGAAAG TATCACCAGA TACATCTAGC AAAAATACTG GGGAAGTGTC      1200
CAGTAATCCT AGTGATTGCA CAACCTCAGT TGGAGAATCA AATAAACCAG AACATAATGA      1260
CTCTAAAAAT GAAATTCAG AAAAACTGT AGAAGAAGTT CCAGTAAATC CAAATGAAGG      1320
CACAGTAGAA GGTACCTCAA ATCAAGAAAC AGAAAAACCA GTTCAACCTG CAGAAGAAAC      1380
ACAAACAAAC TCTGGGAAAA TAGCTAACGA AAATACTGGA GAAGTATCCA ATAAACCTAG      1440
TGATTCAAAA CCACCAGTTG AAGAATCAAA TCAACCAGAA AAAAACGGAA CTGCAACAAA      1500
ACCAGAAAAT TCAGGTAATA CAACATCAGA GAATGGACAA ACAGAACCAG AACCATCAAA      1560
CGGAAATTCA ACTGAGGATG TTTCAACCGA ATCAAACACA TCCAATTCAA ATGGAAACGA      1620
AGAAATTAAA CAAGAAAATG AACTAGACCC TGATAAAAAG GTAGAAGAAC CAGAGAAAAC      1680
ACTTGAATTA AGAAATGTTT CCGACCTAGA GTTA                                  1714

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Asn Tyr Asn Thr Asp Tyr Glu Leu Thr Ser Gly Glu Lys Leu Pro Leu
1           5           10           15
Pro Lys Glu Ile Ser Gly Tyr Thr Tyr Ile Gly Tyr Ile Lys Glu Gly
20          25          30
Lys Thr Thr Ser Glu Ser Glu Val Ser Asn Gln Lys Ser Ser Val Ala
35          40          45
Thr Pro Thr Lys Gln Gln Lys Val Asp Tyr Asn Val Thr Pro Asn Phe
50          55          60
Val Asp His Pro Ser Thr Val Gln Ala Ile Gln Glu Gln Thr Pro Val
65          70          75          80
Ser Ser Thr Lys Pro Thr Glu Val Gln Val Val Glu Lys Pro Phe Ser
85          90          95
Thr Glu Leu Ile Asn Pro Arg Lys Glu Glu Lys Gln Ser Ser Asp Ser
100         105         110

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Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn Ser
 450 455 460
 Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro Ser
 465 470 475 480
 Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn Gly
 485 490 495
 Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn Gly
 500 505 510
 Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val Ser
 515 520 525
 Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys Gln
 530 535 540
 Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys Thr
 545 550 555 560
 Leu Glu Leu Arg Asn Val Ser Asp Leu Glu Leu
 565 570

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGAGAATCAA GCTACACCCA AAGAGACTAG CGCTCAAAAG ACAATCGTCC TTGCTACAGC	60
TGGCGACGTG CCACCATTG ACTACGAAGA CAAGGGCAAT CTGACAGGCT TTGATATCGA	120
AGTTTTAAAG GCAGTAGATG AAAAAGCTCAG CGACTACGAG ATTCAATTCC AAAGAACCGC	180
CTGGGAGAGC ATCTTCCCAG GACTTGATTC TGGTCACTAT CAGGCTGCGG CCAATAACTT	240
GAGTTACACA AAAGAGCGTG CTGAAAAATA CCTTTACTCG CTTCCAATTT CCAACAATCC	300
CCTCGTCCTT GTCAGCAACA AGAAAAATCC TTTGACTTCT CTTGACCAGA TCGCTGGTAA	360
AACAACACAA GAGGATACCG GAACTTCTAA CGCTCAATTC ATCAATAACT GGAATCAGAA	420
ACACACTGAT AATCCCGCTA CAATTAATTT TTCTGGTGAG GATATTGGTA AACGAATCCT	480
AGACCTTGCT AACGGAGAGT TTGATTTCTT AGTTTTTGAC AAGGTATCCG TTCAAAAGAT	540
TATCAAGGAC CGTGGTTTTAG ACCTCTCAGT CGTTGATTTA CCTTCTGCAG ATAGCCCCAG	600
CAATTATATC ATTTTCTCAA GCGACCAAAA AGAGTTTAAA GAGCAATTTG ATAAAGCGCT	660
CAAAGAACTC TATCAAGACG GAACCCTTGA AAAACTCAGC AATACCTATC TAGGTGGTTC	720
TTACCTCCCA GATCAATCTC AGTTACAA	748

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile Val
 1 5 10 15
 Leu Ala Thr Ala Gly Asp Val Pro Pro Phe Asp Tyr Glu Asp Lys Gly
 20 25 30
 Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu Lys
 35 40 45
 Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser Ile
 50 55 60
 Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Ala Asn Asn Leu
 65 70 75 80
 Ser Tyr Thr Lys Glu Arg Ala Glu Lys Tyr Leu Tyr Ser Leu Pro Ile
 85 90 95
 Ser Asn Asn Pro Leu Val Leu Val Ser Asn Lys Lys Asn Pro Leu Thr
 100 105 110
 Ser Leu Asp Gln Ile Ala Gly Lys Thr Thr Gln Glu Asp Thr Gly Thr
 115 120 125
 Ser Asn Ala Gln Phe Ile Asn Asn Trp Asn Gln Lys His Thr Asp Asn
 130 135 140
 Pro Ala Thr Ile Asn Phe Ser Gly Glu Asp Ile Gly Lys Arg Ile Leu
 145 150 155 160
 Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val Ser
 165 170 175
 Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val Asp
 180 185 190
 Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser Asp
 195 200 205
 Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu Tyr
 210 215 220
 Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly Ser
 225 230 235 240
 Tyr Leu Pro Asp Gln Ser Gln Leu Gln
 -----245

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGGTAACCGC TCTTCTCGTA ACGCAGCTTC ATCTTCTGAT GTGAAGACAA AAGCAGCAAT 60
 CGTCACTGAT ACTGGTGGTG TTGATGACAA ATCATTCAAC CAATCAGCTT GGAAGGTTT 120
 GCAGGCTTGG GGTAAAGAAC ACAATCTTTC AAAAGATAAC GGTTCCTACTT ACTTCCAATC 180
 AACAAAGTGA GCTGACTACG CTAACAACCTT GCAACAAGCG GCTGGAAGTT ACAACCTAAT 240
 CTTGGGTGTT GGTTCCTGCCC TTAATAATGC AGTTAAAGAT GCAGCAAAAAG AACACACTGA 300
 CTTGAAGTAT GTCTTGATTG ATGATGTGAT TAAAGACCAA AAGAATGTTG CGAGCGTAAC 360
 TTTGCTGAT AATGAGTCAG GTTACCTTGC AGGTGTGGCT GCAGCAAAAA CAACTAAGAC 420
 AAAACAAGTT GGTTCCTGTAG GTGGTATCGA ATCTGAAGTT ATCTCTCGTT TTGAAGCAGG 480
 ATTCAAGGCT GGTGTTGCGT CAGTAGACCC ATCTATCAAA GTCCAAGTTG ACTACGCTGG 540
 TTCATTTGGT GATGCGGCTA AAGGTAAAAC AATTGCAGCC GCACAATACG CAGCCGGTGC 600
 AGATATTGTT TACCAAGTAG CTGGTGGTAC AGGTGCAGGT GTCTTTGCAG AGGCAAAATC 660
 TCTCAACGAA AGCCGTCTCTG AAAATGAAAA AGTTTGGGTT ATCGGTGTTG ATCGTGACCA 720
 AGAAGCAGAA GGTAAATACA CTTCTAAAGA TGGCAAAGAA TCAAACCTTTG TTCTTGATATC 780
 TACTTTGAAA CAAGTTGGTA CAACTGTAAA AGATATTTCT AACAAGGCAG AAAGAGGAGA 840
 ATTCCCTGGC GGTCAAGTGA TCGTTTACTC ATTGAAGGAT AAAGGGGTTG ACTTGGCAGT 900
 AACAAACCTT TCAGAAGAAG GTAAAAAAGC TGTCGAAGAT GCAAAAGCTA AAATCCTTGA 960
 TGGAAGCGTA AAAGTTCCTG AAAAA 985

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser Ser Ser Asp Val Lys Thr
 1 5 10 15
 Lys Ala Ala Ile Val Thr Asp Thr Gly Gly Val Asp Asp Lys Ser Phe
 20 25 30
 Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Glu His Asn

35	40	45
Leu Ser Lys Asp Asn Gly Phe Thr Tyr Phe Gln Ser Thr Ser Glu Ala		
50	55	60
Asp Tyr Ala Asn Asn Leu Gln Gln Ala Ala Gly Ser Tyr Asn Leu Ile		
65	70	75 80
Phe Gly Val Gly Phe Ala Leu Asn Asn Ala Val Lys Asp Ala Ala Lys		
	85	90 95
Glu His Thr Asp Leu Asn Tyr Val Leu Ile Asp Asp Val Ile Lys Asp		
	100	105 110
Gln Lys Asn Val Ala Ser Val Thr Phe Ala Asp Asn Glu Ser Gly Tyr		
	115	120 125
Leu Ala Gly Val Ala Ala Ala Lys Thr Thr Lys Thr Lys Gln Val Gly		
	130	135 140
Phe Val Gly Gly Ile Glu Ser Glu Val Ile Ser Arg Phe Glu Ala Gly		
	145	150 155 160
Phe Lys Ala Gly Val Ala Ser Val Asp Pro Ser Ile Lys Val Gln Val		
	165	170 175
Asp Tyr Ala Gly Ser Phe Gly Asp Ala Ala Lys Gly Lys Thr Ile Ala		
	180	185 190
Ala Ala Gln Tyr Ala Ala Gly Ala Asp Ile Val Tyr Gln Val Ala Gly		
	195	200 205
Gly Thr Gly Ala Gly Val Phe Ala Glu Ala Lys Ser Leu Asn Glu Ser		
	210	215 220
Arg Pro Glu Asn Glu Lys Val Trp Val Ile Gly Val Asp Arg Asp Gln		
	225	230 235 240
Glu Ala Glu Gly Lys Tyr Thr Ser Lys Asp Gly Lys Glu Ser Asn Phe		
	245	250 255
Val Leu Val Ser Thr Leu Lys Gln Val Gly Thr Thr Val Lys Asp Ile		
	260	265 270
Ser Asn Lys Ala Glu Arg Gly Glu Phe Pro Gly Gly Gln Val Ile Val		
	275	280 285
Tyr Ser Leu Lys Asp Lys Gly Val Asp Leu Ala Val Thr Asn Leu Ser		
	290	295 300
Glu Glu Gly Lys Lys Ala Val Glu Asp Ala Lys Ala Lys Ile Leu Asp		
	305	310 315 320
Gly Ser Val Lys Val Pro Glu Lys		
	325	

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGCTGATT CAGGTGACAA ACCTGTTATC	60
AAAATGTACC AAATCGGTGA CAAACCAGAC AACTTGATG AATTGTTAGC AAATGCCAAC	120
AAAATCATTG AAGAAAAAGT TGGTGCCAAA TTGGATATCC AATACCTTGG CTGGGGTGAC	180
TATGGTAAGA AAATGTCAGT TATCACATCA TCTGGTGAAA ACTATGATAT TGCCTTTGCA	240
GATAACTATA TTGTAAATGC TCAAAAAGGT GCTTACGCTG ACTTGACAGA ATTGTACAAA	300
AAAGAAGGTA AAGACCTTTA CAAAGCACTT GACCCAGCTT ACATCAAGGG TAATACTGTA	360
AATGGTAAGA TTTACGCTGT TCCAGTTGCA GCCAACGTTG CATCATCTCA AACTTTGCC	420
TTCAACGGAA CTCTCCTTGC TAAATATGGT ATCGATATTT CAGGTGTTAC TTCTTACGAA	480
ACTCTTGAGC CAGTCTTGAA ACAAATCAAA GAAAAAGCTC CAGACGTAGT ACCATTTGCT	540
ATTGGTAAAG TTTTCATCCC ATCTGATAAT TTTGACTACC CAGTAGCAAA CGGTCTTCCA	600
TTCGTTATCG ACCTTGAAGG CGATACTACT AAAGTTGTAA ACCGTTACGA AGTGCCTCGT	660
TTCAAAGAAC ACTTGAAGAC TCTTCACAAA TTCTATGAAG CTGGCTACAT TCCAAAAGAC	720
GTCGCAACAA GCGATACTTC CTTTGACCTT CAACAAGATA CTTGGTTCGT TCGTGAAGAA	780
ACAGTAGGAC CAGCTGACTA CGGTAACAGC TTGCTTTCAC GTGTTGCCAA CAAAGATATC	840
CAAATCAAAC CAATTACTAA CTTCATCAAG NAAAACCAAA CAACACAAGT TGCTAACTTT	900
GTCATCTCAA ACAACTCTAA GAACAAAGAA AAATCAATGG AAATCTTGAA CCTCTTGAAT	960
ACGAACCCAG AACTCTTGAA CGGTCTTGTT TACGGTCCAG AAGGCAAGAA CTGGGAAAAA	1020
ATTGAAGGTA AAGAAAACCG GTTTCGCGTT CTTGATGGCT ACAAAGGAAA CACTCACATG	1080
GGTGGATGGA AACTGGTAA CAACTGGATC CTTTACATCA ACGAAAACGT TACAGACCAA	1140
CAAATCGAAA ATTCTAAGAA AGAATTGGCA GAAGCTAAAG AATCTCCAGC GCTTGGATTT	1200
ATCTTCAATA CTGACAATGT GAAATCTGAA ATCTCAGCTA TTGCTAACAC AATGCAACAA	1260
TTTGATACAG CTATCAACAC TGGTACTGTA GACCCAGATA AAGCGATTCC AGAATTGATG	1320
GAAAAATTGA AATCTGAAGG TGCCTACGAA AAAGTATTGA ACGAAATGCA AAAACAATAC	1380
GATGAATTCT TGAAAAACAA AAAA	1404

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Cys 1	Gly	Asn	Leu	Thr 5	Gly	Asn	Ser	Lys	Lys 10	Ala	Ala	Asp	Ser	Gly 15	Asp
Lys	Pro	Val	Ile 20	Lys	Met	Tyr	Gln	Ile 25	Gly	Asp	Lys	Pro	Asp 30	Asn	Leu
Asp	Glu	Leu 35	Leu	Ala	Asn	Ala	Asn 40	Lys	Ile	Ile	Glu	Glu 45	Lys	Val	Gly
Ala	Lys 50	Leu	Asp	Ile	Gln	Tyr 55	Leu	Gly	Trp	Gly	Asp 60	Tyr	Gly	Lys	Lys
Met 65	Ser	Val	Ile	Thr	Ser 70	Ser	Gly	Glu	Asn	Tyr 75	Asp	Ile	Ala	Phe	Ala 80
Asp	Asn	Tyr	Ile 85	Val	Asn	Ala	Gln	Lys	Gly 90	Ala	Tyr	Ala	Asp	Leu 95	Thr
Glu	Leu	Tyr	Lys 100	Lys	Glu	Gly	Lys	Asp 105	Leu	Tyr	Lys	Ala	Leu 110	Asp	Pro
Ala	Tyr 115	Ile	Lys	Gly	Asn	Thr 120	Val	Asn	Gly	Lys	Ile	Tyr 125	Ala	Val	Pro
Val 130	Ala	Ala	Asn	Val	Ala	Ser 135	Ser	Gln	Asn	Phe	Ala 140	Phe	Asn	Gly	Thr
Leu 145	Leu	Ala	Lys	Tyr	Gly 150	Ile	Asp	Ile	Ser	Gly 155	Val	Thr	Ser	Tyr	Glu 160
Thr	Leu	Glu	Pro 165	Val	Leu	Lys	Gln	Ile 170	Lys	Glu	Lys	Ala	Pro	Asp 175	Val
Val	Pro	Phe 180	Ala	Ile	Gly	Lys	Val	Phe 185	Ile	Pro	Ser	Asp	Asn 190	Phe	Asp
Tyr	Pro 195	Val	Ala	Asn	Gly	Leu	Pro 200	Phe	Val	Ile	Asp	Leu 205	Glu	Gly	Asp
Thr 210	Thr	Lys	Val	Val	Asn	Arg 215	Tyr	Glu	Val	Pro	Arg 220	Phe	Lys	Glu	His
Leu 225	Lys	Thr	Leu	His	Lys 230	Phe	Tyr	Glu	Ala	Gly 235	Tyr	Ile	Pro	Lys	Asp 240
Val	Ala	Thr	Ser 245	Asp	Thr	Ser	Phe	Asp	Leu 250	Gln	Gln	Asp	Thr	Trp 255	Phe
Val	Arg	Glu 260	Glu	Thr	Val	Gly	Pro	Ala 265	Asp	Tyr	Gly	Asn	Ser 270	Leu	Leu
Ser	Arg 275	Val	Ala	Asn	Lys	Asp	Ile 280	Gln	Ile	Lys	Pro	Ile 285	Thr	Asn	Phe
Ile 290	Lys	Xaa	Asn	Gln	Thr	Thr 295	Gln	Val	Ala	Asn	Phe 300	Val	Ile	Ser	Asn
Asn 305	Ser	Lys	Asn	Lys	Glu 310	Lys	Ser	Met	Glu	Ile 315	Leu	Asn	Leu	Leu	Asn 320
Thr	Asn	Pro	Glu	Leu	Leu	Asn	Gly	Leu	Val	Tyr	Gly	Pro	Glu	Gly	Lys

325

330

335

Asn Trp Glu Lys Ile Glu Gly Lys Glu Asn Arg Val Arg Val Leu Asp
 340 345 350
 Gly Tyr Lys Gly Asn Thr His Met Gly Gly Trp Asn Thr Gly Asn Asn
 355 360 365
 Trp Ile Leu Tyr Ile Asn Glu Asn Val Thr Asp Gln Gln Ile Glu Asn
 370 375 380
 Ser Lys Lys Glu Leu Ala Glu Ala Lys Glu Ser Pro Ala Leu Gly Phe
 385 390 395 400
 Ile Phe Asn Thr Asp Asn Val Lys Ser Glu Ile Ser Ala Ile Ala Asn
 405 410 415
 Thr Met Gln Gln Phe Asp Thr Ala Ile Asn Thr Gly Thr Val Asp Pro
 420 425 430
 Asp Lys Ala Ile Pro Glu Leu Met Glu Lys Leu Lys Ser Glu Gly Ala
 435 440 445
 Tyr Glu Lys Val Leu Asn Glu Met Gln Lys Gln Tyr Asp Glu Phe Leu
 450 455 460
 Lys Asn Lys Lys
 465

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGGTCAAGGA ACTGCTTCTA AAGACAACAA AGAGGCAGAA CTTAAGAAGG TTGACTTTAT	60
CCTAGACTGG ACACCAAATA CCAACCACAC AGGGCTTTAT GTTGCCAAGG AAAAAGGTTA	120
TTTCAAAGAA GCTGGAGTGG ATGTTGATTT GAAATTGCCA CCAGAAGAAA GTTCTTCTGA	180
CTTGGTATC AACGGAAAGG CACCATTTGC AGTGTATTTT CAAGACTACA TGGCTAAGAA	240
ATTGGAAGAA GGAGCAGGAA TCACTGCCGT TGCAGCTATT GTTGAACACA ATACATCAGG	300
AATCATCTCT CGTAAATCTG ATAATGTAAG CAGTCCAAAA GACTTG GTTG GTAAGAAATA	360
TGGGACATGG AATGACCCAA CTGAACTTGC TATGTTGAAA ACCTTG GTTAG AATCTCAAGG	420
TGGAGACTTT GAGAAGGTTG AAAAAGTACC AAATAACGAC TCAAAC TCAA TCACACCGAT	480
TGCCAATGGC GTCTTTGATA CTGCTTGGAT TTACTACGGT TGGGATGGTA TCCTTGCTAA	540
ATCTCAAGGT GTAGATGCTA ACTTCATGTA CTTGAAAGAC TATGTCAAGG AGTTTGACTA	600
CTATTCACCA GTTATCATCG CAAACAACGA CTATCTGAAA GATAACAAAG AAGAAGCTCG	660
CAAAGTCATC CAAGCCATCA AAAAAGGCTA CCAATATGCC ATGGAACATC CAGAAGAAGC	720

TGCAGATATT CTCATCAAGA ATGCACCTGA ACTCAAGGAA AAACGTGACT TTGTCATCGA 780
 ATCTCAAAAA TACTTGTCAA AAGAATACGC AAGCGACAAG GAAAAATGGG GTCAATTTGA 840
 CGCAGCTCGC TGAATGCTT TCTACAAATG GGATAAAGAA AATGGTATCC TTAAAGAAGA 900
 CTTGACAGAC AAAGGCTTCA CCAACGAATT TGTGAAA 937

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly	Gln	Gly	Thr	Ala	Ser	Lys	Asp	Asn	Lys	Glu	Ala	Glu	Leu	Lys	Lys	1	5	10	15
Val	Asp	Phe	Ile	Leu	Asp	Trp	Thr	Pro	Asn	Thr	Asn	His	Thr	Gly	Leu	20	25	30	
Tyr	Val	Ala	Lys	Glu	Lys	Gly	Tyr	Phe	Lys	Glu	Ala	Gly	Val	Asp	Val	35	40	45	
Asp	Leu	Lys	Leu	Pro	Pro	Glu	Glu	Ser	Ser	Ser	Asp	Leu	Val	Ile	Asn	50	55	60	
Gly	Lys	Ala	Pro	Phe	Ala	Val	Tyr	Phe	Gln	Asp	Tyr	Met	Ala	Lys	Lys	65	70	75	80
Leu	Glu	Lys	Gly	Ala	Gly	Ile	Thr	Ala	Val	Ala	Ala	Ile	Val	Glu	His	85	90	95	
Asn	Thr	Ser	Gly	Ile	Ile	Ser	Arg	Lys	Ser	Asp	Asn	Val	Ser	Ser	Pro	100	105	110	
Lys	Asp	Leu	Val	Gly	Lys	Lys	Tyr	Gly	Thr	Trp	Asn	Asp	Pro	Thr	Glu	115	120	125	
Leu	Ala	Met	Leu	Lys	Thr	Leu	Val	Glu	Ser	Gln	Gly	Gly	Asp	Phe	Glu	130	135	140	
Lys	Val	Glu	Lys	Val	Pro	Asn	Asn	Asp	Ser	Asn	Ser	Ile	Thr	Pro	Ile	145	150	155	160
Ala	Asn	Gly	Val	Phe	Asp	Thr	Ala	Trp	Ile	Tyr	Tyr	Gly	Trp	Asp	Gly	165	170	175	
Ile	Leu	Ala	Lys	Ser	Gln	Gly	Val	Asp	Ala	Asn	Phe	Met	Tyr	Leu	Lys	180	185	190	
Asp	Tyr	Val	Lys	Glu	Phe	Asp	Tyr	Tyr	Ser	Pro	Val	Ile	Ile	Ala	Asn	195	200	205	
Asn	Asp	Tyr	Leu	Lys	Asp	Asn	Lys	Glu	Glu	Ala	Arg	Lys	Val	Ile	Gln	210	215	220	

[illegible]

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAGCTCAGGT	GGAAACGCTG	GTTTCATCCTC	TGGAAAAACA	ACTGCCAAAG	CTCGCACTAT	60
CGATGAAATC	AAAAAAGCG	GTGAAGTGC	AATCGCCGTG	TTTGGAGATA	AAAAACCGTT	120
TGGCTACGTT	GACAATGATG	GTTCTACCAA	GGTACGCTAC	GATATTGAAC	TAGGGAACCA	180
ACTAGCTCAA	GACCTTGGTG	TCAAGGTTAA	ATACATTTCA	GTCGATGCTG	CCAACCGTGC	240
GGAATACTTG	ATTTCAAACA	AGGTAGATAT	TACTCTTGCT	AACTTTACAG	TAAGTACGA	300
ACGTAAGAAA	CAAGTTGATT	TTGCCCTTCC	ATATATGAAA	GTTTCTCTGG	GTGTCGTATC	360
ACCTAAGACT	GGTCTCATTA	CAGACGTCAA	ACAAGTTGAA	GGTAAACCT	TAATTGTCAC	420
AAAAGGA	ACTGCTGAGA	CTTATTTTGA	AAAGAATCAT	CCAGAAATCA	AACTCCAAAA	480
ATACGACCAA	TACAGTGACT	CTTACCAAGC	TCTTCTTGAC	GGACGTGGAG	ATGCCTTTTC	540
AACTGACAAT	ACGGAAGTTC	TAGCTTGGGC	GCTTGAAAAT	AAAGGATTTG	AAGTAGGAAT	600
TACTTCCCTC	GGTGATCCCG	ATACCATTGC	GGCAGCAGTT	CAAAAAGGCA	ACCAAGAATT	660
GCTAGACTTC	ATCAATAAAG	ATATTGAAAA	ATTAGGCAAG	GAAACTTCT	TCCACAAGGC	720
CTATGAAAAG	ACACTTCACC	CAACCTACGG	TGACGCTGCT	AAAGCAGATG	ACCTGGTTGT	780
TGAAGGTGGA	AAAGTTGAT					799

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Ser Ser Gly Gly Asn Ala Gly Ser Ser Ser Gly Lys Thr Thr Ala Lys
1      5      10      15
Ala Arg Thr Ile Asp Glu Ile Lys Lys Ser Gly Glu Leu Arg Ile Ala
20      25      30
Val Phe Gly Asp Lys Lys Pro Phe Gly Tyr Val Asp Asn Asp Gly Ser
35      40      45
Thr Lys Val Arg Tyr Asp Ile Glu Leu Gly Asn Gln Leu Ala Gln Asp
50      55      60
Leu Gly Val Lys Val Lys Tyr Ile Ser Val Asp Ala Ala Asn Arg Ala
65      70      75      80
Glu Tyr Leu Ile Ser Asn Lys Val Asp Ile Thr Leu Ala Asn Phe Thr
85      90      95
Val Thr Asp Glu Arg Lys Lys Gln Val Asp Phe Ala Leu Pro Tyr Met
100     105     110
Lys Val Ser Leu Gly Val Val Ser Pro Lys Thr Gly Leu Ile Thr Asp
115     120     125
Val Lys Gln Leu Glu Gly Lys Thr Leu Ile Val Thr Lys Gly Thr Thr
130     135     140
Ala Glu Thr Tyr Phe Glu Lys Asn His Pro Glu Ile Lys Leu Gln Lys
145     150     155     160
Tyr Asp Gln Tyr Ser Asp Ser Tyr Gln Ala Leu Leu Asp Gly Arg Gly
165     170     175
Asp Ala Phe Ser Thr Asp Asn Thr Glu Val Leu Ala Trp Ala Leu Glu
180     185     190
Asn Lys Gly Phe Glu Val Gly Ile Thr Ser Leu Gly Asp Pro Asp Thr
195     200     205
Ile Ala Ala Ala Val Gln Lys Gly Asn Gln Glu Leu Leu Asp Phe Ile
210     215     220
Asn Lys Asp Ile Glu Lys Leu Gly Lys Glu Asn Phe Phe His Lys Ala
225     230     235     240
Tyr Glu Lys Thr Leu His Pro Thr Tyr Gly Asp Ala Ala Lys Ala Asp
245     250     255
Asp Leu Val Val Glu Gly Gly Lys Val Asp
260     265

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(2) -INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCCAACATAT GGTAAATCTG CGGATGGCAC AGTGACCATC GAGTATTTCA ACCAGAAAAA	60
AGAAATGACC AAAACCTTGG AAGAAATCAC TCGTGATTTT GAGAAGGAAA ACCCTAAGAT	120
CAAGGTCAAA GTCGTCAATG TACCAAATGC TGGTGAAGTA TTGAAGACAC GCGTTCTCGC	180
AGGAGATGTG CCTGATGTGG TCAATATTTA CCCACAGTCC ATCGAACTGC AAGAATGGGC	240
AAAAGCAGGT GTTTTTGAAG ATTTGAGCAA CAAAGACTAC CTGAAACGCG TGAAAAATGG	300
CTACGCTGAA AAATATGCTG TAAACGAAAA AGTTTACAAC GTTCCTTTTA CAGCTAATGC	360
TTATGGAATT TACTACAACA AAGATAAATT CGAAGAACTG GGCTTGAAGG TTCCTGAAAC	420
CTGGGATGAA TTTGAACAGT TAGTCAAAGA TATCGTTGCT AAAGGACAAA CACCATTG	480
AATTGCAGGT GCAGATGCTT GGACACTCAA TGGTTACAAT CAATTAGCCT TTGCGACAGC	540
AACAGGTGGA GGAAAAGAAG CAAATCAATA CCTTCGTTAT TCTCAACCAA ATGCCATTAA	600
ATTGTCGGAT CCGATTATGA AAGATGATAT CAAGGTCATG GACATCCTTC GCATCAATGG	660
ATCTAAGCAA AAGAACTGGG AAGGTGCTGG CTATACCGAT GTTATCGGAG CCTTCGCACG	720
TGGGGATGTC CTCATGACAC CAAATGGGTC TTGGGCGATC ACAGCGATTA ATGAACAAAA	780
ACCGAACTTT AAGATTGGGA CCTTCATGAT TCCAGGAAAA GAAAAAGGAC AAAGCTTAAC	840
CGTTGGTGCG GGAGACTTGG CATGGTCTAT CTCAGCCACC ACCAAACATC CAAAAGAAGC	900
CAATGCCTTT GTGGAATATA TGACCCGTCC AGAAGTCATG CAAAAATACT ACGATGTGGA	960
CGGATCTCCA ACAGCGATCG AAGGGGTCAA ACAAGCAGGA GAAGATTACG CGCTTGCTGG	1020
TATGACCGAA TATGCCTTTA CGGATCGTCA CTTGGTCTGG TTGCAACAAT ACTGGACCAG	1080
TGAAGCAGAC TTCCATACCT TGACCATGAA CTATGTCTTG ACCGGTGATA AACAAGGCAT	1140
GGTCAATGAT TTGAATGCCT TCTTTAACCC GATGAAAGCG GATGTGGAT	1189

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser	Asn	Tyr	Gly	Lys	Ser	Ala	Asp	Gly	Thr	Val	Thr	Ile	Glu	Tyr	Phe
1				5					10					15	

Asn	Gln	Lys	Lys	Glu	Met	Thr	Lys	Thr	Leu	Glu	Glu	Ile	Thr	Arg	Asp
			20					25					30		
Phe	Glu	Lys	Glu	Asn	Pro	Lys	Ile	Lys	Val	Lys	Val	Val	Asn	Val	Pro
		35					40					45			
Asn	Ala	Gly	Glu	Val	Leu	Lys	Thr	Arg	Val	Leu	Ala	Gly	Asp	Val	Pro
	50					55					60				
Asp	Val	Val	Asn	Ile	Tyr	Pro	Gln	Ser	Ile	Glu	Leu	Gln	Glu	Trp	Ala
65					70					75					80
Lys	Ala	Gly	Val	Phe	Glu	Asp	Leu	Ser	Asn	Lys	Asp	Tyr	Leu	Lys	Arg
				85					90					95	
Val	Lys	Asn	Gly	Tyr	Ala	Glu	Lys	Tyr	Ala	Val	Asn	Glu	Lys	Val	Tyr
			100					105					110		
Asn	Val	Pro	Phe	Thr	Ala	Asn	Ala	Tyr	Gly	Ile	Tyr	Tyr	Asn	Lys	Asp
		115					120					125			
Lys	Phe	Glu	Glu	Leu	Gly	Leu	Lys	Val	Pro	Glu	Thr	Trp	Asp	Glu	Phe
	130					135					140				
Glu	Gln	Leu	Val	Lys	Asp	Ile	Val	Ala	Lys	Gly	Gln	Thr	Pro	Phe	Gly
145					150					155					160
Ile	Ala	Gly	Ala	Asp	Ala	Trp	Thr	Leu	Asn	Gly	Tyr	Asn	Gln	Leu	Ala
				165					170					175	
Phe	Ala	Thr	Ala	Thr	Gly	Gly	Gly	Lys	Glu	Ala	Asn	Gln	Tyr	Leu	Arg
			180					185					190		
Tyr	Ser	Gln	Pro	Asn	Ala	Ile	Lys	Leu	Ser	Asp	Pro	Ile	Met	Lys	Asp
		195					200					205			
Asp	Ile	Lys	Val	Met	Asp	Ile	Leu	Arg	Ile	Asn	Gly	Ser	Lys	Gln	Lys
	210					215					220				
Asn	Trp	Glu	Gly	Ala	Gly	Tyr	Thr	Asp	Val	Ile	Gly	Ala	Phe	Ala	Arg
225					230					235					240
Gly	Asp	Val	Leu	Met	Thr	Pro	Asn	Gly	Ser	Trp	Ala	Ile	Thr	Ala	Ile
				245					250					255	
Asn	Glu	Gln	Lys	Pro	Asn	Phe	Lys	Ile	Gly	Thr	Phe	Met	Ile	Pro	Gly
			260					265					270		
Lys	Glu	Lys	Gly	Gln	Ser	Leu	Thr	Val	Gly	Ala	Gly	Asp	Leu	Ala	Trp
		275					280					285			
Ser	Ile	Ser	Ala	Thr	Thr	Lys	His	Pro	Lys	Glu	Ala	Asn	Ala	Phe	Val
	290					295					300				
Glu	Tyr	Met	Thr	Arg	Pro	Glu	Val	Met	Gln	Lys	Tyr	Tyr	Asp	Val	Asp
305					310					315					320
Gly	Ser	Pro	Thr	Ala	Ile	Glu	Gly	Val	Lys	Gln	Ala	Gly	Glu	Asp	Ser
				325					330					335	
Pro	Leu	Ala	Gly	Met	Thr	Glu	Tyr	Ala	Phe	Thr	Asp	Arg	His	Leu	Val
			340					345					350		

Trp Leu Gln Gln Tyr Trp Thr Ser Glu Ala Asp Phe His Thr Leu Thr
 355 360 365

Met Asn Tyr Val Leu Thr Gly Asp Lys Gln Gly Met Val Asn Asp Leu
 370 375 380

Asn Ala Phe Phe Asn Pro Met Lys Ala Asp Val Asp
 385 390 395

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TGGGAAAAAT TCTAGCGAAA CTAGTGGAGA TAATTGGTCA AAGTACCAGT CTAACAAGTC	60
TATTACTATT GGATTGATA GTACTTTTGT TCCAATGGGA TTTGCTCAGA AAGATGGTTC	120
TTATGCAGGA TTTGATATTG ATTTAGCTAC AGCTGTTTTT GAAAAATACG GAATCACGGT	180
AAATTGGCAA CCGATTGATT GGGATTTGAA AGAAGCTGAA TTGACAAAAG GAACGATTGA	240
TCTGATTTGG AATGGCTATT CCGCTACAGA CGAACGCCGT GAAAAGGTGG CTTTCAGTAA	300
CTCATATATG AAGAATGAGC AGGTATTGGT TACGAAGAAA TCATCTGGTA TCACGACTGC	360
AAAGGATATG ACTGGAAAGA CATTAGGAGC TCAAGCTGGT TCATCTGGTT ATGCGGACTT	420
TGAAGCAAAT CCAGAAATTT TGAAGAATAT TGTCGCTAAT AAGGAAGCGA ATCAATACCA	480
AACCTTTAAT GAAGCCTTGA TTGATTTGAA AAACGATCGA ATTGATGGTC TATTGATTGA	540
CCGTGTCTAT GCAAACTATT ATTTAGAAGC AGAAGGTGTT TTAAACGATT ATAATGTCTT	600
TACAGTTGGA CTAGAAACAG AAGCTTTTGC GGTGAGGCC CGTAAGGAAG ATACAAACTT	660
GGTTAAGAAG ATAAATGAAG CTTTTTCTAG TCTTTACAAG GACGGCAAGT TCCAAGAAAT	720
CAGCCAAAAA TGGTTTGGAG AAGATGTAGC AACCAAAGAA GTAAAAGAAG GACAG	775

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Lys Asn Ser Ser Glu Thr Ser Gly Asp Asn Trp Ser Lys Tyr Gln	
1 5 10 15	
Ser Asn Lys Ser Ile Thr Ile Gly Phe Asp Ser Thr Phe Val Pro Met	

131

20	25	30
Gly Phe Ala Gln Lys Asp Gly Ser Tyr Ala Gly Phe Asp Ile Asp Leu 35 40 45		
Ala Thr Ala Val Phe Glu Lys Tyr Gly Ile Thr Val Asn Trp Gln Pro 50 55 60		
Ile Asp Trp Asp Leu Lys Glu Ala Glu Leu Thr Lys Gly Thr Ile Asp 65 70 75 80		
Leu Ile Trp Asn Gly Tyr Ser Ala Thr Asp Glu Arg Arg Glu Lys Val 85 90 95		
Ala Phe Ser Asn Ser Tyr Met Lys Asn Glu Gln Val Leu Val Thr Lys 100 105 110		
Lys Ser Ser Gly Ile Thr Thr Ala Lys Asp Met Thr Gly Lys Thr Leu 115 120 125		
Gly Ala Gln Ala Gly Ser Ser Gly Tyr Ala Asp Phe Glu Ala Asn Pro 130 135 140		
Glu Ile Leu Lys Asn Ile Val Ala Asn Lys Glu Ala Asn Gln Tyr Gln 145 150 155 160		
Thr Phe Asn Glu Ala Leu Ile Asp Leu Lys Asn Asp Arg Ile Asp Gly 165 170 175		
Leu Leu Ile Asp Arg Val Tyr Ala Asn Tyr Tyr Leu Glu Ala Glu Gly 180 185 190		
Val Leu Asn Asp Tyr Asn Val Phe Thr Val Gly Leu Glu Thr Glu Ala 195 200 205		
Phe Ala Val Gly Ala Arg Lys Glu Asp Thr Asn Leu Val Lys Lys Ile 210 215 220		
Asn Glu Ala Phe Ser Ser Leu Tyr Lys Asp Gly Lys Phe Gln Glu Ile 225 230 235 240		
Ser Gln Lys Trp Phe Gly Glu Asp Val Ala Thr Lys Glu Val Lys Glu 245 250 255		
Gly Gln		

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 868 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGCTAGCGGA AAAAAAGATA CAACTTCTGG TCAAAACTA AAAGTTGTTG CTACAACTC	60
AATCATCGCT GATATTACTA AAAATATTGC TGGTGACAAA ATTGACCTTC ATAGTATCGT	120

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TCCGATTGGG CAAGACCCAC ACGAATACGA ACCACTTCCT GAAGACGTTA AGAAAACTTC      180
TGAGGCTAAT TTGATTTTCT ATAACGGTAT CAACCTTGAA ACAGGTGGCA ATGCTTGGTT      240
TACAAAATTG GTAGAAAATG CCAAGAAAAC TGAAAACAAA GACTACTTCG CAGTCAGCGA      300
CGGCGTTGAT GTTATCTACC TTGAAGGTCA AAATGAAAAA GGAAAAGAAG ACCCACACGC      360
TTGGCTTAAC CTTGAAAACG GTATTATTTT TGCTAAAAAT ATCGCCAAAC AATTGAGCGC      420
CAAAGACCCT AACAATAAAG AATTCTATGA AAAAAATCTC AAAGAATATA CTGATAAGTT      480
AGACAAACTT GATAAAGAAA GTAAGGATAA ATTTAATAAG ATCCCTGCTG AAAAGAAACT      540
CATTGTAACC AGCGAAGGAG CATTCAAATA CTTCTCTAAA GCCTATGGTG TCCCAAGTGC      600
TTACATCTGG GAAATCAATA CTGAAGAAGA AGGAACTCCT GAACAAATCA AGACCTTGGT      660
TGAAAAACTT CGCCAAACAA AAGTTCCATC ACTCTTTGTA GAATCAAGTG TGGATGACCG      720
TCCAATGAAA ACTGTTTCTC AAGACACAAA CATCCCAATC TACGCTCAA TCTTTACTGA      780
CTCTATCGCA GAACAAGGTA AAGAAGGCGA CAGCTACTAC AGCATGATGA AATACAACCT      840
TGACAAGATT GCTGAAGGAT TGGCAAAA      868

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(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 289 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Ala Ser Gly Lys Lys Asp Thr Thr Ser Gly Gln Lys Leu Lys Val Val
1           5           10           15

Ala Thr Asn Ser Ile Ile Ala Asp Ile Thr Lys Asn Ile Ala Gly Asp
20           25           30

Lys Ile Asp Leu His Ser Ile Val Pro Ile Gly Gln Asp Pro His Glu
35           40           45

Tyr Glu Pro Leu Pro Glu Asp Val Lys Lys Thr Ser Glu Ala Asn Leu
50           55           60

Ile Phe Tyr Asn Gly Ile Asn Leu Glu Thr Gly Gly Asn Ala Trp Phe
65           70           75           80

Thr Lys Leu Val Glu Asn Ala Lys Lys Thr Glu Asn Lys Asp Tyr Phe
85           90           95

Ala Val Ser Asp Gly Val Asp Val Ile Tyr Leu Glu Gly Gln Asn Glu
100          105          110

Lys Gly Lys Glu Asp Pro His Ala Trp Leu Asn Leu Glu Asn Gly Ile
115          120          125

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Ile Phe Ala Lys Asn Ile Ala Lys Gln Leu Ser Ala Lys Asp Pro Asn
 130 135 140

Asn Lys Glu Phe Tyr Glu Lys Asn Leu Lys Glu Tyr Thr Asp Lys Leu
 145 150 155 160

Asp Lys Leu Asp Lys Glu Ser Lys Asp Lys Phe Asn Lys Ile Pro Ala
 165 170 175

Glu Lys Lys Leu Ile Val Thr Ser Glu Gly Ala Phe Lys Tyr Phe Ser
 180 185 190

Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile Trp Glu Ile Asn Thr Glu
 195 200 205

Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr Leu Val Glu Lys Leu Arg
 210 215 220

Gln Thr Lys Val Pro Ser Leu Phe Val Glu Ser Ser Val Asp Asp Arg
 225 230 235 240

Pro Met Lys Thr Val Ser Gln Asp Thr Asn Ile Pro Ile Tyr Ala Gln
 245 250 255

Ile Phe Thr Asp Ser Ile Ala Glu Gln Gly Lys Glu Gly Asp Ser Tyr
 260 265 270

Tyr Ser Met Met Lys Tyr Asn Leu Asp Lys Ile Ala Glu Gly Leu Ala
 275 280 285

Lys

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGGCTCAAAA AATACAGCTT CAAGTCCAGA TTATAAGTTG GAAGGTGTAA CATTCCCGCT	60
TCAAGAAAAG AAAACATTGA AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAAGACCC	120
AAATGAAAAG TTAATTTTGC AACGTTTGGA GAAGGAAACT GGC GTTCATA TTGACTGGAC	180
CAACTACCAA TCCGACTTTG CAGAAAAACG TAACTTGGAT ATTTCTAGTG GTGATTTACC	240
AGATGCTATC CACAACGACG GAGCTTCAGA TGTGGACTTG ATGAACTGGG CTAAAAAAGG	300
TGTTATTATT CCAGTTGAAG ATTTGATTGA TAAATACATG CCAAATCTTA AGAAAATTTT	360
GGATGAGAAA CCAGAGTACA AGGCCTTGAT GACAGCACCT GATGGGCACA TTTACTCATT	420
TCCATGGATT GAAGAGCTTG GAGATGGTAA AGAGTCTATT CACAGTGTCA ACGATATGGC	480
TTGGATTAAC AAAGATTGGC TTAAGAAACT TGGTCTTGAA ATGCCAAAAA CTACTGATGA	540

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TTTGATTAAA GTCCTAGAAG CTTTCAAAAA CGGGGATCCA AATGGAAATG GAGAGGCTGA      600
TGAAATTCCA TTTTCATTTA TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTGC      660
TGCATTTGGT ATAGGGGATA ACGATGATCA TTTAGTAGTA GGAAATGATG GCAAAGTTGA      720
CTTCACAGCA GATAACGATA ACTATAAAGA AGGTGTCAAA TTTATCCGTC AATTGCAAGA      780
AAAAGGCCTG ATTGATAAAG AAGCTTTTCGA ACATGATTGG AATAGTTACA TTGCTAAAGG      840
TCATGATCAG AAATTTGGTG TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA      900
CGAAAGTTAT GATGTTTTAC CAGTACTTGC TGGACCAAGT GGTCAAAAAC ACGTAGCTCG      960
TACAAACGGT ATGGGATTTG CACGTGACAA GATGGTTATT ACCAGTGTA AAAAAACCT      1020
AGAATTGACA GCTAAATGGA TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATAA      1080
CTGGGGAACT TACGGAGATG ACAAACAACA AAACATCTTT GAATTGGATC AAGCGTCAAA      1140
TAGTCTAAAA CACTTACCAC TAAACGGAAC TGCACCAGCA GAACTTCGTC AAAAGACTGA      1200
AGTAGGAGGA CCACTAGCTA TCCTAGATTC ATACTATGGT AAAGTAACAA CCATGCCTGA      1260
TGATGCCAAA TGGCGTTTGG ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT      1320
CAATAACTAT CCAAGAGTCT TTATGACACA GGAAGATTTG GACAAGATTG CCCATATCGA      1380
AGCAGATATG AATGACTATA TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT      1440
TGATACTGAG TGGGATGATT ACAAGAAAGA ACTTGAAAAA TACGGACTTT CTGATTACCT      1500
CGCTATTAAA CAAAATACT ACGACCAATA CCAAGCAAAC AAAAAC      1546

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Gly Ser Lys Asn Thr Ala Ser Ser Pro Asp Tyr Lys Leu Glu Gly Val
1           5           10           15

Thr Phe Pro Leu Gln Glu Lys Lys Thr Leu Lys Phe Met Thr Ala Ser
20           25           30

Ser Pro Leu Ser Pro Lys Asp Pro Asn Glu Lys Leu Ile Leu Gln Arg
35           40           45

Leu Glu Lys Glu Thr Gly Val His Ile Asp Trp Thr Asn Tyr Gln Ser
50           55           60

Asp Phe Ala Glu Lys Arg Asn Leu Asp Ile Ser Ser Gly Asp Leu Pro
65           70           75           80

Asp Ala Ile His Asn Asp Gly Ala Ser Asp Val Asp Leu Met Asn Trp

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85

90

95

Ala	Lys	Lys	Gly	Val	Ile	Ile	Pro	Val	Glu	Asp	Leu	Ile	Asp	Lys	Tyr
			100					105					110		
Met	Pro	Asn	Leu	Lys	Lys	Ile	Leu	Asp	Glu	Lys	Pro	Glu	Tyr	Lys	Ala
		115					120					125			
Leu	Met	Thr	Ala	Pro	Asp	Gly	His	Ile	Tyr	Ser	Phe	Pro	Trp	Ile	Glu
	130					135					140				
Glu	Leu	Gly	Asp	Gly	Lys	Glu	Ser	Ile	His	Ser	Val	Asn	Asp	Met	Ala
145					150					155					160
Trp	Ile	Asn	Lys	Asp	Trp	Leu	Lys	Lys	Leu	Gly	Leu	Glu	Met	Pro	Lys
				165					170					175	
Thr	Thr	Asp	Asp	Leu	Ile	Lys	Val	Leu	Glu	Ala	Phe	Lys	Asn	Gly	Asp
			180					185					190		
Pro	Asn	Gly	Asn	Gly	Glu	Ala	Asp	Glu	Ile	Pro	Phe	Ser	Phe	Ile	Ser
		195					200					205			
Gly	Asn	Gly	Asn	Glu	Asp	Phe	Lys	Phe	Leu	Phe	Ala	Ala	Phe	Gly	Ile
	210					215					220				
Gly	Asp	Asn	Asp	Asp	His	Leu	Val	Val	Gly	Asn	Asp	Gly	Lys	Val	Asp
225					230					235					240
Phe	Thr	Ala	Asp	Asn	Asp	Asn	Tyr	Lys	Glu	Gly	Val	Lys	Phe	Ile	Arg
				245					250					255	
Gln	Leu	Gln	Glu	Lys	Gly	Leu	Ile	Asp	Lys	Glu	Ala	Phe	Glu	His	Asp
			260					265					270		
Trp	Asn	Ser	Tyr	Ile	Ala	Lys	Gly	His	Asp	Gln	Lys	Phe	Gly	Val	Tyr
		275					280					285			
Phe	Thr	Trp	Asp	Lys	Asn	Asn	Val	Thr	Gly	Ser	Asn	Glu	Ser	Tyr	Asp
	290					295					300				
Val	Leu	Pro	Val	Leu	Ala	Gly	Pro	Ser	Gly	Gln	Lys	His	Val	Ala	Arg
305					310					315					320
Thr	Asn	Gly	Met	Gly	Phe	Ala	Arg	Asp	Lys	Met	Val	Ile	Thr	Ser	Val
				325					330					335	
Asn	Lys	Asn	Leu	Glu	Leu	Thr	Ala	Lys	Trp	Ile	Asp	Ala	Gln	Tyr	Ala
			340					345					350		
Pro	Leu	Gln	Ser	Val	Gln	Asn	Asn	Trp	Gly	Thr	Tyr	Gly	Asp	Asp	Lys
		355					360					365			
Gln	Gln	Asn	Ile	Phe	Glu	Leu	Asp	Gln	Ala	Ser	Asn	Ser	Leu	Lys	His
	370					375					380				
Leu	Pro	Leu	Asn	Gly	Thr	Ala	Pro	Ala	Glu	Leu	Arg	Gln	Lys	Thr	Glu
385					390					395					400
Val	Gly	Gly	Pro	Leu	Ala	Ile	Leu	Asp	Ser	Tyr	Tyr	Gly	Lys	Val	Thr
				405					410					415	
Thr	Met	Pro	Asp	Asp	Ala	Lys	Trp	Arg	Leu	Asp	Leu	Ile	Lys	Glu	Tyr

420	425	430
Tyr Val Pro Tyr Met Ser Asn Val Asn Asn Tyr Pro Arg Val Phe Met 435 440 445		
Thr Gln Glu Asp Leu Asp Lys Ile Ala His Ile Glu Ala Asp Met Asn 450 455 460		
Asp Tyr Ile Tyr Arg Lys Arg Ala Glu Trp Ile Val Asn Gly Asn Ile 465 470 475 480		
Asp Thr Glu Trp Asp Asp Tyr Lys Lys Glu Leu Glu Lys Tyr Gly Leu 485 490 495		
Ser Asp Tyr Leu Ala Ile Lys Gln Lys Tyr Tyr Asp Gln Tyr Gln Ala 500 505 510		
Asn Lys Asn 515		

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 895 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TAGTACAAAC TCAAGCACTA GTCAGACAGA GACCAGTAGC TCTGCTCCAA CAGAGGTAAC	60
CATTAAAAGT TCACTGGACG AGGTCAAACCT TTCCAAAGTT CCTGAAAAGA TTGTGACCTT	120
TGACCTCGGC GCTGCGGATA CTATTCGCGC TTTAGGATTT GAAAAAATA TCGTCGGAAT	180
GCCTACAAAA ACTGTTCCGA CTTATCTAAA AGACCTAGTG GGAAGTGTCA AAAATGTTGG	240
TTCTATGAAA GAACCTGATT TAGAAGCTAT CGCCGCCCTT GAGCCTGATT TGATTATCGC	300
TTCGCCACGT ACACAAAAAT TCGTAGACAA ATTCAAAGAA ATCGCCCCAA CCGTTCTCTT	360
CCAAGCAAGC AAGGACGACT ACTGGACTTC TACCAAGGCT AATATCGAAT CCTTAGCAAG	420
TGCCTTCGGC GAAACTGGTA CACAGAAAGC CAAGGAAGAA TTGACCAAGC TAGACAAGAG	480
CATCCAAGAA GTCGCTACTA AAAATGAAAG CTCTGACAAA AAAGCCCTTG CGATCCTCCT	540
TAATGAAGGA AAAATGGCAG CCTTTGGTGC CAAATCTCGT TTCTCTTTCT TGTACCAAAC	600
CTTGAAATTC AAACCAACTG ATACAAAATT TGAAGACTCA CGCCACGGAC AAGAAGTCAG	660
CTTTGAAAGT GTCAAAGAAA TCAACCCTGA CATCCTCTTT GTCATCAACC GTACCCTTGC	720
CATCGGTGGG GACAACTCTA GCAACGACGG TGTCTAGAA AATGCCCTTA TCGCTGAAAC	780
ACCTGCTGCT AAAAATGGTA AGATTATCCA ACTAACACCA GACCTCTGGT ATCTAAGCGG	840
AGGCGGACTT GAATCAACAA AACTCATGAT TGAAGACATA CAAAAAGCTT TGAAA	895

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 298 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser	Thr	Asn	Ser	Ser	Thr	Ser	Gln	Thr	Glu	Thr	Ser	Ser	Ser	Ala	Pro	1	5	10	15
Thr	Glu	Val	Thr	Ile	Lys	Ser	Ser	Leu	Asp	Glu	Val	Lys	Leu	Ser	Lys	20	25	30	
Val	Pro	Glu	Lys	Ile	Val	Thr	Phe	Asp	Leu	Gly	Ala	Ala	Asp	Thr	Ile	35	40	45	
Arg	Ala	Leu	Gly	Phe	Glu	Lys	Asn	Ile	Val	Gly	Met	Pro	Thr	Lys	Thr	50	55	60	
Val	Pro	Thr	Tyr	Leu	Lys	Asp	Leu	Val	Gly	Thr	Val	Lys	Asn	Val	Gly	65	70	75	80
Ser	Met	Lys	Glu	Pro	Asp	Leu	Glu	Ala	Ile	Ala	Ala	Leu	Glu	Pro	Asp	85	90	95	
Leu	Ile	Ile	Ala	Ser	Pro	Arg	Thr	Gln	Lys	Phe	Val	Asp	Lys	Phe	Lys	100	105	110	
Glu	Ile	Ala	Pro	Thr	Val	Leu	Phe	Gln	Ala	Ser	Lys	Asp	Asp	Tyr	Trp	115	120	125	
Thr	Ser	Thr	Lys	Ala	Asn	Ile	Glu	Ser	Leu	Ala	Ser	Ala	Phe	Gly	Glu	130	135	140	
Thr	Gly	Thr	Gln	Lys	Ala	Lys	Glu	Glu	Leu	Thr	Lys	Leu	Asp	Lys	Ser	145	150	155	160
Ile	Gln	Glu	Val	Ala	Thr	Lys	Asn	Glu	Ser	Ser	Asp	Lys	Lys	Ala	Leu	165	170	175	
Ala	Ile	Leu	Leu	Asn	Glu	Gly	Lys	Met	Ala	Ala	Phe	Gly	Ala	Lys	Ser	180	185	190	
Arg	Phe	Ser	Phe	Leu	Tyr	Gln	Thr	Leu	Lys	Phe	Lys	Pro	Thr	Asp	Thr	195	200	205	
Lys	Phe	Glu	Asp	Ser	Arg	His	Gly	Gln	Glu	Val	Ser	Phe	Glu	Ser	Val	210	215	220	
Lys	Glu	Ile	Asn	Pro	Asp	Ile	Leu	Phe	Val	Ile	Asn	Arg	Thr	Leu	Ala	225	230	235	240
Ile	Gly	Gly	Asp	Asn	Ser	Ser	Asn	Asp	Gly	Val	Leu	Glu	Asn	Ala	Leu	245	250	255	
Ile	Ala	Glu	Thr	Pro	Ala	Ala	Lys	Asn	Gly	Lys	Ile	Ile	Gln	Leu	Thr	260	265	270	

Pro 'Asp Leu Trp Tyr Leu Ser Gly Gly Gly Leu Glu Ser Thr Lys Leu
 275 280 285

Met Ile Glu Asp Ile Gln Lys Ala Leu Lys
 290 295

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TGGCAATTCT GGC GGAAGTA AAGATGCTGC CAAATCAGGT GGTGACGGTG CAAAACAGA	60
AATCACTTGG TGGGCATTCC CAGTATTTAC CCAAGAAAAA ACTGGTGACG GTGTTGGAAC	120
TTATGAAAAA TCAATCATCG AAGCGTTTGA AAAAGCAAAC CCAGATATAA AAGTGAAATT	180
GGAAACCATC GACTTCAAGT CAGGTCTCTGA AAAAATCACA ACAGCCATCG AAGCAGGAAC	240
AGCTCCAGAC GTACTCTTTG ATGCACCAGG ACGTATCATC CAATACGGTA AAAACGGTAA	300
ATTGGCTGAG TTGAATGACC TCTTCACAGA TGAATTTGTT AAAGATGTCA ACAATGAAAA	360
CATCGTACAA GCAAGTAAAG CTGGAGACAA GGCTTATATG TATCCGATTA GTTCTGCCCC	420
ATTCTACATG GCAATGAACA AGAAAATGTT AGAAGATGCT GGAGTAGCAA ACCTTGTAAG	480
AGAAGGTTGG ACAACTGATG ATTTTGAAAA AGTATTGAAA GCACTTAAAG ACAAGGGTTA	540
CACACCAGGT TCATTGTTCA GTTCTGGTCA AGGGGGAGAC CAAGGAACAC GTGCCTTTAT	600
CTCTAACCTT TATAGCGGTT CTGTAACAGA TGAAAAAGTT AGCAAATATA CAACTGATGA	660
TCCTAAATTC GTCAAAGGTC TTGAAAAAGC AACTAGCTGG ATTAAAGACA ATTTGATCAA	720
TAATGGTTCA CAATTTGACG GTGGGGCAGA TATCCAAAAC TTTGCCAACG GTCAAACATC	780
TTACACAATC CTTTGGGCAC CAGCTCAAAA TGGTATCCAA GCTAAACTTT TAGAAGCAAG	840
TAAGGTAGAA GTGGTAGAAG TACCATTCCC ATCAGACGAA GGTAAGCCAG CTCTTGAGTA	900
CCTTGTA AAC GGGTTTG CAG TATTCAACAA TAAAGACGAC AAGAAAGTCG CTGCATCTAA	960
GAAATTCATC CAGTTTATCG CAGATGACAA GGAGTGGGGA CCTAAAGACG TAGTTCGTAC	1020
AGGTGCTTTC CCAGTCCGTA CTTTATTTGG AAAACTTTAT GAAGACAAAC GCATGGAAAC	1080
AATCAGCGGC TGGACTCAAT ACTACTCACC ATACTACAAC ACTATTGATG GATTTGCTGA	1140
AATGAGAACA CTTTGGTTCC CAATGTTGCA ATCTGTATCA AATGGTGACG AAAAACCAGC	1200
AGATGCTTTG AAAGCCTTCA CTGAAAAAGC GAACGAAACA ATCAAAAAAG CTATGAAACA	1260
A	1261

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly	Asn	Ser	Gly	Gly	Ser	Lys	Asp	Ala	Ala	Lys	Ser	Gly	Gly	Asp	Gly	1	5	10	15
Ala	Lys	Thr	Glu	Ile	Thr	Trp	Trp	Ala	Phe	Pro	Val	Phe	Thr	Gln	Glu	20	25	30	
Lys	Thr	Gly	Asp	Gly	Val	Gly	Thr	Tyr	Glu	Lys	Ser	Ile	Ile	Glu	Ala	35	40	45	
Phe	Glu	Lys	Ala	Asn	Pro	Asp	Ile	Lys	Val	Lys	Leu	Glu	Thr	Ile	Asp	50	55	60	
Phe	Lys	Ser	Gly	Pro	Glu	Lys	Ile	Thr	Thr	Ala	Ile	Glu	Ala	Gly	Thr	65	70	75	80
Ala	Pro	Asp	Val	Leu	Phe	Asp	Ala	Pro	Gly	Arg	Ile	Ile	Gln	Tyr	Gly	85	90	95	
Lys	Asn	Gly	Lys	Leu	Ala	Glu	Leu	Asn	Asp	Leu	Phe	Thr	Asp	Glu	Phe	100	105	110	
Val	Lys	Asp	Val	Asn	Asn	Glu	Asn	Ile	Val	Gln	Ala	Ser	Lys	Ala	Gly	115	120	125	
Asp	Lys	Ala	Tyr	Met	Tyr	Pro	Ile	Ser	Ser	Ala	Pro	Phe	Tyr	Met	Ala	130	135	140	
Met	Asn	Lys	Lys	Met	Leu	Glu	Asp	Ala	Gly	Val	Ala	Asn	Leu	Val	Lys	145	150	155	160
Glu	Gly	Trp	Thr	Thr	Asp	Asp	Phe	Glu	Lys	Val	Leu	Lys	Ala	Leu	Lys	165	170	175	
Asp	Lys	Gly	Tyr	Thr	Pro	Gly	Ser	Leu	Phe	Ser	Ser	Gly	Gln	Gly	Gly	180	185	190	
Asp	Gln	Gly	Thr	Arg	Ala	Phe	Ile	Ser	Asn	Leu	Tyr	Ser	Gly	Ser	Val	195	200	205	
Thr	Asp	Glu	Lys	Val	Ser	Lys	Tyr	Thr	Thr	Asp	Asp	Pro	Lys	Phe	Val	210	215	220	
Lys	Gly	Leu	Glu	Lys	Ala	Thr	Ser	Trp	Ile	Lys	Asp	Asn	Leu	Ile	Asn	225	230	235	240
Asn	Gly	Ser	Gln	Phe	Asp	Gly	Gly	Ala	Asp	Ile	Gln	Asn	Phe	Ala	Asn	245	250	255	
Gly	Gln	Thr	Ser	Tyr	Thr	Ile	Leu	Trp	Ala	Pro	Ala	Gln	Asn	Gly	Ile	260	265	270	

Gln Ala Lys Leu Leu Glu Ala Ser Lys Val Glu Val Val Glu Val Pro
 275 280 285
 Phe Pro Ser Asp Glu Gly Lys Pro Ala Leu Glu Tyr Leu Val Asn Gly
 290 295 300
 Phe Ala Val Phe Asn Asn Lys Asp Asp Lys Lys Val Ala Ala Ser Lys
 305 310 315 320
 Lys Phe Ile Gln Phe Ile Ala Asp Asp Lys Glu Trp Gly Pro Lys Asp
 325 330 335
 Val Val Arg Thr Gly Ala Phe Pro Val Arg Thr Ser Phe Gly Lys Leu
 340 345 350
 Tyr Glu Asp Lys Arg Met Glu Thr Ile Ser Gly Trp Thr Gln Tyr Tyr
 355 360 365
 Ser Pro Tyr Tyr Asn Thr Ile Asp Gly Phe Ala Glu Met Arg Thr Leu
 370 375 380
 Trp Phe Pro Met Leu Gln Ser Val Ser Asn Gly Asp Glu Lys Pro Ala
 385 390 395 400
 Asp Ala Leu Lys Ala Phe Thr Glu Lys Ala Asn Glu Thr Ile Lys Lys
 405 410 415
 Ala Met Lys Gln
 420

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 658 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TTCACAAGAA AAAACAAAAA ATGAAGATGG AGAACTAAG ACAGAACAGA CAGCCAAAGC	60
TGATGGAACA GTCGGTAGTA AGTCTCAAGG AGCTGCCCAG AAGAAAGCAG AAGTGGTCAA	120
TAAAGGTGAT TACTACAGCA TTCAAGGGAA ATACGATGAA ATCATCGTAG CCAACAAACA	180
CTATCCATTG TCTAAAGACT ATAATCCAGG GGAAAATCCA ACAGCCAAGG CAGAGTTGGT	240
CAAACATC ATC AAAGCGATGC AAGAGGCAGG TTTCCCTATT AGTGATCATT ACAGTGGTTT	300
TAGAAGTTAT GAAACTCAGA CCAAGCTCTA TCAAGATTAT GTCAACCAAG ATGGAAAGGC	360
AGCAGCTGAC CGTTACTCTG CCCGTCCTGG CTATAGCGAA CACCAGACAG GCTTGGCCTT	420
TGATGTGATT GGGACTGATG GTGATTTGGT GACAGAAGAA AAAGCAGCCC AATGGCTCTT	480
GGATCATGCA GCTGATTATG GCTTTGTTGT CCGTTATCTC AAAGGCAAGG AAAAGGAAAC	540
AGGCTATATG GCTGAAGAAT GGCACCTGCG TTATGTAGGA AAAGAAGCTA AAGAAATTGC	600
TGCAAGTGGT CTCAGTTTGG AAGAATACTA TGGCTTTGAA GGCGGAGACT ACGTCGAT	658

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Ser Gln Glu Lys Thr Lys Asn Glu Asp Gly Glu Thr Lys Thr Glu Gln
1          5          10          15
Thr Ala Lys Ala Asp Gly Thr Val Gly Ser Lys Ser Gln Gly Ala Ala
          20          25          30
Gln Lys Lys Ala Glu Val Val Asn Lys Gly Asp Tyr Tyr Ser Ile Gln
          35          40          45
Gly Lys Tyr Asp Glu Ile Ile Val Ala Asn Lys His Tyr Pro Leu Ser
          50          55          60
Lys Asp Tyr Asn Pro Gly Glu Asn Pro Thr Ala Lys Ala Glu Leu Val
          65          70          75          80
Lys Leu Ile Lys Ala Met Gln Glu Ala Gly Phe Pro Ile Ser Asp His
          85          90          95
Tyr Ser Gly Phe Arg Ser Tyr Glu Thr Gln Thr Lys Leu Tyr Gln Asp
          100          105          110
Tyr Val Asn Gln Asp Gly Lys Ala Ala Ala Asp Arg Tyr Ser Ala Arg
          115          120          125
Pro Gly Tyr Ser Glu His Gln Thr Gly Leu Ala Phe Asp Val Ile Gly
          130          135          140
Thr Asp Gly Asp Leu Val Thr Glu Glu Lys Ala Ala Gln Trp Leu Leu
          145          150          155          160
Asp His Ala Ala Asp Tyr Gly Phe Val Val Arg Tyr Leu Lys Gly Lys
          165          170          175
Glu Lys Glu Thr Gly Tyr Met Ala Glu Glu Trp His Leu Arg Tyr Val
          180          185          190
Gly Lys Glu Ala Lys Glu Ile Ala Ala Ser Gly Leu Ser Leu Glu Glu
          195          200          205
Tyr Tyr Gly Phe Glu Gly Gly Asp Tyr Val Asp
          210          215

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(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GAAAGGTCTG TGGTCAAATA ATCTTACCTG CGGTTATGAT GAAAAAATAA TCTTGGA AAA 60
TATAAATATA AAAATACCTG AAGAAAAAAT ATCAGTTATT ATTGGGTCAA ATGTTGTGG 120
GAAATCAACA CTCATTAAAA CCTGTCTCG ACTTATAAAG CCATTAGAGG GAGAAGTATT 180
GCTTGATAAT AAATCAATTA ATTCTTATAA AGAAAAAGAT TTAGCAAAAC ACATAGCTAT 240
ATTACCTCAA TCTCCAATAA TCCCTGAATC AATAACAGTA GCTGATCTTG TAAGCCGTGG 300
TCGTTTCCCC TACAGAAAGC CTTTAAAGAG TCTTGGA AAA GATGACCTTG AAATAATAAA 360
CAGATCAATG GTTAAGGCCA ATGTTGAAGA TCTAGCAAAT AACCTAGTTG AAGAACTTTC 420
TGGGGGTCAA AGGCAAAGAG TATGGATAGC TCTAGCCCTA GCCCAAGATA CAAGTATCCT 480
ACTTTTAGAT GAGCCAACTA CTTACTTGGA TATCTCATAT CAAATAGAAC TATTAGACCT 540
CTTGACTGAT CTAAACCAA AATATAAGAC AACCATTGTC ATGATTTTGC ACGATATAAA 600
TCTAACAGCA AGATACGCTG ATTACCTATT TGCAATTAAA GAAGGTAAAC TTGTTGCAGA 660
GGGAAAGCCT GAAGATATAC TAAATGATAA ACTAGTTAAA GATATCTTTA ATCTTGAAGC 720
AAAAATTATA CGTGACCCTA TTTCCAATTC GCCTCTAATG ATTCTTATTG GCAAGCACCA 780
TGTTAACTCT 790

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Leu Trp Ser Asn Asn Leu Thr Cys Gly Tyr Asp Glu Lys Ile
1 5 10 15
Ile Leu Glu Asn Ile Asn Ile Lys Ile Pro Glu Glu Lys Ile Ser Val
20 25 30
Ile Ile Gly Ser Asn Gly Cys Gly Lys Ser Thr Leu Ile Lys Thr Leu
35 40 45
Ser Arg Leu Ile Lys Pro Leu Glu Gly Glu Val Leu Leu Asp Asn Lys
50 55 60
Ser Ile Asn Ser Tyr Lys Glu Lys Asp Leu Ala Lys His Ile Ala Ile
65 70 75 80
Leu Pro Gln Ser Pro Ile Ile Pro Glu Ser Ile Thr Val Ala Asp Leu
85 90 95

Val Ser Arg Gly Arg Phe Pro Tyr Arg Lys Pro Phe Lys Ser Leu Gly
 100 105 110
 Lys Asp Asp Leu Glu Ile Ile Asn Arg Ser Met Val Lys Ala Asn Val
 115 120 125
 Glu Asp Leu Ala Asn Asn Leu Val Glu Glu Leu Ser Gly Gly Gln Arg
 130 135 140
 Gln Arg Val Trp Ile Ala Leu Ala Leu Ala Gln Asp Thr Ser Ile Leu
 145 150 155 160
 Leu Leu Asp Glu Pro Thr Thr Tyr Leu Asp Ile Ser Tyr Gln Ile Glu
 165 170 175
 Leu Leu Asp Leu Leu Thr Asp Leu Asn Gln Lys Tyr Lys Thr Thr Ile
 180 185 190
 Cys Met Ile Leu His Asp Ile Asn Leu Thr Ala Arg Tyr Ala Asp Tyr
 195 200 205
 Leu Phe Ala Ile Lys Glu Gly Lys Leu Val Ala Glu Gly Lys Pro Glu
 210 215 220
 Asp Ile Leu Asn Asp Lys Leu Val Lys Asp Ile Phe Asn Leu Glu Ala
 225 230 235 240
 Lys Ile Ile Arg Asp Pro Ile Ser Asn Ser Pro Leu Met Ile Pro Ile
 245 250 255
 Gly Lys His His Val Ser
 260

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 781 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAACTCAGAA AAGAAAGCAG ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG	60
CGGTTCTGAA GAAAAACGTT GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC	120
CTTGGAATTT ACAGAGTTCA CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA	180
AGTAGATTTG AACGCTTTCC AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG	240
AAAAGACCTT GTAGCGATTG CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT	300
GAATGGAAGT GCCAACAAGT AACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC	360
TGTACCGAAT GACGCTACAA ACGAAAGCCG TGCCTTTTAT TTGCTTCAAT CAGCTGGCTT	420
GATTAAATTG GATGTTTCTG GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC	480
AAAGAACTTG AAAATCACTG AATTGGACGC TAGCCAAACA GCTCGTTCAT TGTATCAGT	540

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TGACGCTGCC GTTGTAAACA ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC      600
ACTTTTCAAA GAACAAGCTG ATGAAAATC AAAACAATGG TACAACATCA TTGTTGCAAA      660
AAAAGATTGG GAAACATCAC CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA      720
CACAGATGAC GTGAAAAAAG TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG      780
G                                                                           781

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(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Asn Ser Glu Lys Lys Ala Asp Asn Ala Thr Thr Ile Lys Ile Ala Thr
1           5           10           15
Val Asn Arg Ser Gly Ser Glu Glu Lys Arg Trp Asp Lys Ile Gln Glu
20          25          30
Leu Val Lys Lys Asp Gly Ile Thr Leu Glu Phe Thr Glu Phe Thr Asp
35          40          45
Tyr Ser Gln Pro Asn Lys Ala Thr Ala Asp Gly Glu Val Asp Leu Asn
50          55          60
Ala Phe Gln His Tyr Asn Phe Leu Asn Asn Trp Asn Lys Glu Asn Gly
65          70          75          80
Lys Asp Leu Val Ala Ile Ala Asp Thr Tyr Ile Ser Pro Ile Arg Leu
85          90          95
Tyr Ser Gly Leu Asn Gly Ser Ala Asn Lys Tyr Thr Lys Val Glu Asp
100         105         110
Ile Pro Ala Asn Gly Glu Ile Ala Val Pro Asn Asp Ala Thr Asn Glu
115         120         125
Ser Arg Ala Leu Tyr Leu Leu Gln Ser Ala Gly Leu Ile Lys Leu Asp
130         135         140
Val Ser Gly Thr Ala Leu Ala Thr Val Ala Asn Ile Lys Glu Asn Pro
145         150         155         160
Lys Asn Leu Lys Ile Thr Glu Leu Asp Ala Ser Gln Thr Ala Arg Ser
165         170         175
Leu Ser Ser Val Asp Ala Ala Val Val Asn Asn Thr Phe Val Thr Glu
180         185         190
Ala Lys Leu Asp Tyr Lys Lys Ser Leu Phe Lys Glu Gln Ala Asp Glu
195         200         205

```

Asn Ser Lys Gln Trp Tyr Asn Ile Ile Val Ala Lys Lys Asp Trp Glu
210 215 220

Thr Ser Pro Lys Ala Asp Ala Ile Lys Lys Val Ile Ala Ala Tyr His
225 230 235 240

Thr Asp Asp Val Lys Lys Val Ile Glu Glu Ser Ser Asp Gly Leu Asp
245 250 255

Gln Pro Val Trp
260

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCGAAAGGG TCAGAAGGTG CAGACCTTAT CAGCATGAAA GGGGATGTCA TTACAGAACA	60
TCAATTTTAT GAGCAAGTGA AAAGCAACCC TTCAGCCCCA CAAGTCTTGT TAAATATGAC	120
CATCCAAAAA GTTTTGTGAAA AACAATATGG CTCAGAGCTT GATGATAAAG AGGTTGATGA	180
TACTATTGCC GAAGAAAAAA AACAATATGG CGAAAACTAC CAACGTGTCT TGTCACAAGC	240
AGGTATGACT CTTGAAACAC GTAAAGCTCA AATTCGTACA AGTAAATTAG TTGAGTTGGC	300
AGTTAAGAAG GTAGCAGAAG CTGAATTGAC AGATGAAGCC TATAAGAAAG CCTTTGATGA	360
GTACACTCCA GATGTAACGG CTCAAATCAT CCGTCTTAAT AATGAAGATA AGGCCAAAGA	420
AGTTCTCGAA AAAGCCAAGG CAGAAGGTGC TGATTTTGCT CAATTAGCCA AAGATAATTC	480
AACTGATGAA AAAACAAAAG AAAATGGTGG AGAAATTACC TTTGATTCTG CTTCAACAGA	540
AGTACCTGGA GCAAGTCCAA AAAAGCCGCT TTTCGCTTTT AGATGTGGGA TGGTGTCTTCT	600
GGATGTGGAT TACAGCAACT GGGGCACACC AAGCCTACAG	640

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Lys Gly Ser Glu Gly Ala Asp Leu Ile Ser Met Lys Gly Asp Val
1 5 10 15

Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys Ser Asn Pro Ser Ala

TCCTGTCAGGTC

146

20

25

30

Gln Gln Val Leu Leu Asn Met Thr Ile Gln Lys Val Phe Glu Lys Gln
35 40 45

Tyr Gly Ser Glu Leu Asp Asp Lys Glu Val Asp Asp Thr Ile Ala Glu
50 55 60

Glu Lys Lys Gln Tyr Gly Glu Asn Tyr Gln Arg Val Leu Ser Gln Ala
65 70 75 80

Gly Met Thr Leu Glu Thr Arg Lys Ala Gln Ile Arg Thr Ser Lys Leu
85 90 95

Val Glu Leu Ala Val Lys Lys Val Ala Glu Ala Glu Leu Thr Asp Glu
100 105 110

Ala Tyr Lys Lys Ala Phe Asp Glu Tyr Thr Pro Asp Val Thr Ala Gln
115 120 125

Ile Ile Arg Leu Asn Asn Glu Asp Lys Ala Lys Glu Val Leu Glu Lys
130 135 140

Ala Lys Ala Glu Gly Ala Asp Phe Ala Gln Leu Ala Lys Asp Asn Ser
145 150 155 160

Thr Asp Glu Lys Thr Lys Glu Asn Gly Gly Glu Ile Thr Phe Asp Ser
165 170 175

Ala Ser Thr Glu Val Pro Gly Ala Ser Pro Lys Lys Pro Leu Phe Ala
180 185 190

Phe Arg Cys Gly Met Val Phe Leu Asp Val Asp Tyr Ser Asn Trp Gly
195 200 205

Thr Pro Ser Leu Gln
210

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 631 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA TTGCTCAAAC	60
TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG CTGTTTCAGTG	120
TACAGAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAAACT AAAGCTACGG TTGTAGAAAA	180
ACCACTGAAA GATTTTtagag CGTCTACGTC TGATCAGTCT GGTGGGTGG AATCTAATGG	240
TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA CAGATGGTAA	300
ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAAT TTTCTGGTAG	360
CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTTACAGGC TGGGGAACAG ATGGTAGCAG	420

ATGGTTCTAC TTTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG AAAATGGCAC 480
 TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG TCGGACCACA 540
 CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC CAGATGGTTA 600
 CCGTGTAAT GGTAAATGGTG AATGGGTAAA C 631

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Met Ala Ala Phe Lys Asn Pro Asn Asn Gln Tyr Lys Ala Ile Thr
 1 5 10 15
 Ile Ala Gln Thr Leu Gly Asp Asp Ala Ser Ser Glu Glu Leu Ala Gly
 20 25 30
 Arg Tyr Gly Ser Ala Val Gln Cys Thr Glu Val Thr Ala Ser Asn Leu
 35 40 45
 Ser Thr Val Lys Thr Lys Ala Thr Val Val Glu Lys Pro Leu Lys Asp
 50 55 60
 Phe Arg Ala Ser Thr Ser Asp Gln Ser Gly Trp Val Glu Ser Asn Gly
 65 70 75 80
 Lys Trp Tyr Phe Tyr Glu Ser Gly Asp Val Lys Thr Gly Trp Val Lys
 85 90 95
 Thr Asp Gly Lys Trp Tyr Tyr Leu Asn Asp Leu Gly Val Met Gln Thr
 100 105 110
 Gly Phe Val Lys Phe Ser Gly Ser Trp Tyr Tyr Leu Ser Asn Ser Gly
 115 120 125
 Ala Met Phe Thr Gly Trp Gly Thr Asp Gly Ser Arg Trp Phe Tyr Phe
 130 135 140
 Asp Gly Ser Gly Ala Met Lys Thr Gly Trp Tyr Lys Glu Asn Gly Thr
 145 150 155 160
 Trp Tyr Tyr Leu Asp Glu Ala Gly Ile Met Lys Thr Gly Trp Phe Lys
 165 170 175
 Val Gly Pro His Trp Tyr Tyr Ala Tyr Gly Ser Gly Ala Leu Ala Val
 180 185 190
 Ser Thr Thr Thr Pro Asp Gly Tyr Arg Val Asn Gly Asn Gly Glu Trp
 195 200 205
 Val Asn
 210

102370-123960

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGACGAGCAA AAAATTAAGC AAGCAGAAGC GGAAGTTGAG AGTAAACAAG CTGAGGCTAC	60
AAGGTTAAAA AAAATCAAGA CAGATCGTGA AGAAGCAGAA GAAGAAGCTA AACGAAGAGC	120
AGATGCTAAA GAGCAAGGTA AACCAAAGGG GCGGGCAAAA CGAGGAGTTC CTGGAGAGCT	180
AGCAACACCT GATAAAAAAG AAAATGATGC GAAGTCTTCA GATTCTAGCG TAGGTGAAGA	240
AACTCTTCCA AGCCCATCCC TGAAACCAGA AAAAAAGGTA GCAGAAGCTG AGAAGAAGGT	300
TGAAGAAGCT AAGAAAAAAG CCGAGGATCA AAAAGAAGAA GATCGCCGTA ACTACCCAAC	360
CAATACTTAC AAAACGCTTG AACTTGAAAT TGCTGAGTCC GATGTGGAAG TTAAAAAAGC	420
GGAGCTTGAA CTAGTAAAAG AGGAAGCTAA GGAACCTCGA AACGAGGAAA AAGTTAAGCA	480
AGCAAAAGCG GAAGTTGAGA GTAAAAAAGC TGAGGCTACA AGGTTAGAAA AAATCAAGAC	540
AGATCGTAAA AAAGCAGAAG AAGAAGCTAA ACGAAAAGCA GCAGAAGAAG ATAAAGTTAA	600
AGAAAAACCA GCTGAACAAC CACAACCAGC GCCGGCTCCA AAAGCAGAAA AACCAGCTCC	660
AGCTCCAAAA CCAGAGAATC CAGCTGAACA ACCAAAAGCA GAAAAACCAG CTGATCAACA	720
AGCTGAAGAA GACTATGCTC GTAGATCAGA AGAAGAATAT AATCGCTTGA CTCAACAGCA	780
ACCGCCAAAA ACTGAAAAAC CAGCACAACC ATCTACTCCA AAAACAGGCT GGAAACAAGA	840
AAACGGTATG TGGTACTTCT ACAATACTGA TGGTTCAATG GCGACAGGAT GGCTCCAAAA	900
CAATGGCTCA TGGTACTACC TCAACAGCAA TGGCGCTATG GCGACAGGAT GGCTCCAAAA	960
CAATGGTTCA TGGTACTATC TAAACGCTAA TGGTTCAATG GCAACAGGAT GGCTCCAAAA	1020
CAATGGTTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1080
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1140
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTGATATG GCGACAGGTT GGGTGAAAGA	1200
TGGAGATACC TGGTACTATC TTGAAGCATC AGGTGCTATG AAAGCAAGCC AATGGTTCAA	1260
AGTATCAGAT AAATGGTACT ATGTCAATGG CTCAGGTGCC CTTGCAGTCA ACACAACTGT	1320
AGATGGCTAT GGAGTCAATG CCAATGGTGA ATGGGTAAAC	1360

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids

(ii) MOLECULE TYPE: protein

Asp 1	Glu	Gln	Lys	Ile	Lys	Gln	Ala	Glu	Ala	Glu	Val	Glu	Ser	Lys	Gln	
				5						10					15	
Ala	Glu	Ala	Thr	Arg	Leu	Lys	Lys	Ile	Lys	Thr	Asp	Arg	Glu	Glu	Ala	
			20					25					30			
Glu	Glu	Glu	Ala	Lys	Arg	Arg	Ala	Asp	Ala	Lys	Glu	Gln	Gly	Lys	Pro	
		35					40					45				
Lys	Gly	Arg	Ala	Lys	Arg	Gly	Val	Pro	Gly	Glu	Leu	Ala	Thr	Pro	Asp	
	50					55					60					
Lys	Lys	Glu	Asn	Asp	Ala	Lys	Ser	Ser	Asp	Ser	Ser	Val	Gly	Glu	Glu	
65					70					75					80	
Thr	Leu	Pro	Ser	Pro	Ser	Leu	Lys	Pro	Glu	Lys	Lys	Val	Ala	Glu	Ala	
			85						90					95		
Glu	Lys	Lys	Val	Glu	Glu	Ala	Lys	Lys	Lys	Ala	Glu	Asp	Gln	Lys	Glu	
			100					105					110			
Glu	Asp	Arg	Arg	Asn	Tyr	Pro	Thr	Asn	Thr	Tyr	Lys	Thr	Leu	Glu	Leu	
		115					120					125				
Glu	Ile	Ala	Glu	Ser	Asp	Val	Glu	Val	Lys	Lys	Ala	Glu	Leu	Glu	Leu	
	130					135					140					
Val	Lys	Glu	Glu	Ala	Lys	Glu	Pro	Arg	Asn	Glu	Glu	Lys	Val	Lys	Gln	
145					150					155					160	
Ala	Lys	Ala	Glu	Val	Glu	Ser	Lys	Lys	Ala	Glu	Ala	Thr	Arg	Leu	Glu	
			165						170					175		
Lys	Ile	Lys	Thr	Asp	Arg	Lys	Lys	Ala	Glu	Glu	Glu	Ala	Lys	Arg	Lys	
			180					185					190			
Ala	Ala	Glu	Glu	Asp	Lys	Val	Lys	Glu	Lys	Pro	Ala	Glu	Gln	Pro	Gln	
		195					200					205				
Pro	Ala	Pro	Ala	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Pro	Ala	Pro	Lys	Pro	
	210					215					220					
Glu	Asn	Pro	Ala	Glu	Gln	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Asp	Gln	Gln	
225					230					235					240	
Ala	Glu	Glu	Asp	Tyr	Ala	Arg	Arg	Ser	Glu	Glu	Glu	Tyr	Asn	Arg	Leu	
			245						250					255		
Thr	Gln	Gln	Gln	Pro	Pro	Lys	Thr	Glu	Lys	Pro	Ala	Gln	Pro	Ser	Thr	
			260					265					270			
Pro	Lys	Thr	Gly	Trp	Lys	Gln	Glu	Asn	Gly	Met	Trp	Tyr	Phe	Tyr	Asn	
		275				280						285				

Thr Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp
 290 295 300
 Tyr Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Asn
 305 310 315 320
 Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser Met Ala Thr Gly
 325 330 335
 Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser
 340 345 350
 Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn
 355 360 365
 Ala Asn Gly Ser Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp
 370 375 380
 Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Val Lys Asp
 385 390 395 400
 Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser
 405 410 415
 Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Ser Gly
 420 425 430
 Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Gly Val Asn Ala Asn
 435 440 445
 Gly Glu Trp Val Asn
 450

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGTGGTGAG GAAGAACTA AAAAGACTCA AGCAGCACAA CAGCCAAAAC AACAAACGAC	60
TGTACAACAA ATTGCTGTTG GAAAAGATGC TCCAGACTTC ACATTGCAAT CCATGGATGG	120
CAAAGAAGTT AAGTTATCTG ATTTTAAGGG TAAAAAGGTT TACTTGAAGT TTTGGGCTTC	180
ATGGTGTGGT CCATGCAAGA AAAGTATGCC AGAGTTGATG GAACTAGCGG CGAAACCAGA	240
TCGTGATTTC GAAATTCTTA CTGTCATTGC ACCAGGAATT CAAGGTGAAA AAAGTGTGTA	300
GCAATTCCCA CAATGGTTCC AGGAACAAGG ATATAAGGAT ATCCCAGTTC TTTATGATAC	360
CAAAGCAACC ACTTCCAAGC TTATCAAATT CGAAGCATTC CTACAGAATA TT	412

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Cys Gly Glu Glu Glu Thr Lys Lys Thr Gln Ala Ala Gln Gln Pro Lys
1           5           10           15

Gln Gln Thr Thr Val Gln Gln Ile Ala Val Gly Lys Asp Ala Pro Asp
          20           25           30

Phe Thr Leu Gln Ser Met Asp Gly Lys Glu Val Lys Leu Ser Asp Phe
          35           40           45

Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp Cys Gly Pro
50           55           60

Cys Lys Lys Ser Met Pro Glu Leu Met Glu Leu Ala Ala Lys Pro Asp
65           70           75           80

Arg Asp Phe Glu Ile Leu Thr Val Ile Ala Pro Gly Ile Gln Gly Glu
          85           90           95

Lys Thr Val Glu Gln Phe Pro Gln Trp Phe Gln Glu Gln Gly Tyr Lys
          100          105          110

Asp Ile Pro Val Leu Tyr Asp Thr Lys Ala Thr Thr Ser Lys Leu Ile
          115          120          125

Lys Phe Glu Ala Phe Leu Gln Asn Ile
          130          135
  
```

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

GACTTTTAAC AATAAAACTA TTGAAGAGTT GCACAATCTC CTTGTCTCTA AGGAAATTTT      60
TGCAACAGAA TTGACCCAAG CAACACTTGA AAATATCAAG TCTCGTGAGG AAGCCCTCAA      120
TTCATTTGTC ACCATCGCTG AGGAGCAAGC TCTTGTTCAA GCTAAAGCCA TTGATGAAGC      180
tGGAATTGAT GCTGACAATG TCCTTTCAGG AATTCCACTT GCTGTTAAGG ATAACATCTC      240
TACAGACGGT ATTCTCACAA CTGCTGCCTC AAAAATGCTC TACAACTATG AGCCAATCTT      300
TGATGCGACa gCTgTTGCCA ATGCAAAAAC CAAGGGCATG ATTGTCGTTG GAAAGACCAA      360
CATGGACGAA TTTGCTATGG GTGGTTCAGG tGAAACTTCA CACTACGGAG CAACTAAAAA      420
CGCTTGGAAC CACAGCAAGG TTCCTGGTGG GTCATCAAGT GGTTCGCGG CAGCTGTAGC      480
  
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CTCAGGACAA GTTCGCTTGT CACTTGGTTC TGATACTGGT GGTTCATCC GCCAACCTGC 540
 TGCCTTCAAC GGAATCGTTG GTCTCAAACC AACCTACGGA ACAGTTTCAC GTTTCGGTCT 600
 CATTGCCTTT GGTAGCTCAT TAGACCAGAT TGGACCTTTT GCTCCTACTG TTAAGGAAAA 660
 TGCCCTCTTG CTCAACGCTA TTGCCAGCGA AGATGCTAAA GACTCTACTT CTGCTCCTGT 720
 CCGCATCGCC GACTTTACTT CAAAAATCGG CCAAGACATC AAGGGTATGA AAATCGCTTT 780
 GCCTAAGGAA TACCTAGGCG AAGGAATTGA TCCAGAGGTT AAGGAAACAA TCTTAAACGC 840
 GGCCAAACAC TTTGAAAAAT TGGGTGCTAT CGTCGAAGAA GTCAGCCTTC CTCACTCTAA 900
 ATACGGTGTT GCCGTTTATT ACATCATCGC TTCATCAGAA GCTTCATCAA ACTTGCAACG 960
 CTTCGACGGT ATCCGTTACG GCTATCGCGC AGAAGATGCA ACCAACCTTG ATGAAATCTA 1020
 TGTAACAGC CGAAGCCAAG GTTTTGGTGA AGAGGTAAAA CGTCGTATCA TGCTGGGTAC 1080
 TTTCAGTCTT TCATCAGGTT ACTATGATGC CTACTACAAA AAGGCTGGTC AAGTCCGTAC 1140
 CCTCATCATT CAAGATTTTCG AAAAAGTCTT CGCGGATTAC GATTTGATTT TGGGTCCAAC 1200
 TGCTCCAAGT GTTGCCTATG ACTTGGATTG TCTCAACCAT GACCCAGTTG CCATGTACTT 1260
 AGCCGACCTA TTGACCATAC CTGTAAACTT GGCAGGACTG CCTGGAATTT CGATTCTCTG 1320
 TGGATTCTCT CAAGGTCTAC CTGTCGGACT CCAATTGATT GGTCCCAAGT ACTCTGAGGA 1380
 AACCATTTAC CAAGCTGCTG CTGCTTTTGA AGCAACAACA GACTACCACA AACAACAACC 1440
 CGTGATTTTT GGAGGTGACA AC 1462

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 487 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Phe Asn Asn Lys Thr Ile Glu Glu Leu His Asn Leu Leu Val Ser
 1 5 10 15
 Lys Glu Ile Ser Ala Thr Glu Leu Thr Gln Ala Thr Leu Glu Asn Ile
 20 25 30
 Lys Ser Arg Glu Glu Ala Leu Asn Ser Phe Val Thr Ile Ala Glu Glu
 35 40 45
 Gln Ala Leu Val Gln Ala Lys Ala Ile Asp Glu Ala Gly Ile Asp Ala
 50 55 60
 Asp Asn Val Leu Ser Gly Ile Pro Leu Ala Val Lys Asp Asn Ile Ser
 65 70 75 80

Thr	Asp	Gly	Ile	Leu	Thr	Thr	Ala	Ala	Ser	Lys	Met	Leu	Tyr	Asn	Tyr	
				85					90				95			
Glu	Pro	Ile	Phe	Asp	Ala	Thr	Ala	Val	Ala	Asn	Ala	Lys	Thr	Lys	Gly	
				100					105				110			
Met	Ile	Val	Val	Gly	Lys	Thr	Asn	Met	Asp	Glu	Phe	Ala	Met	Gly	Gly	
				115					120				125			
Ser	Gly	Glu	Thr	Ser	His	Tyr	Gly	Ala	Thr	Lys	Asn	Ala	Trp	Asn	His	
				130					135				140			
Ser	Lys	Val	Pro	Gly	Gly	Ser	Ser	Ser	Gly	Ser	Ala	Ala	Ala	Val	Ala	
				145					150				155			
Ser	Gly	Gln	Val	Arg	Leu	Ser	Leu	Gly	Ser	Asp	Thr	Gly	Gly	Ser	Ile	
				165					170				175			
Arg	Gln	Pro	Ala	Ala	Phe	Asn	Gly	Ile	Val	Gly	Leu	Lys	Pro	Thr	Tyr	
				180					185				190			
Gly	Thr	Val	Ser	Arg	Phe	Gly	Leu	Ile	Ala	Phe	Gly	Ser	Ser	Leu	Asp	
				195					200				205			
Gln	Ile	Gly	Pro	Phe	Ala	Pro	Thr	Val	Lys	Glu	Asn	Ala	Leu	Leu	Leu	
				210					215				220			
Asn	Ala	Ile	Ala	Ser	Glu	Asp	Ala	Lys	Asp	Ser	Thr	Ser	Ala	Pro	Val	
				225					230				235			
Arg	Ile	Ala	Asp	Phe	Thr	Ser	Lys	Ile	Gly	Gln	Asp	Ile	Lys	Gly	Met	
				245					250				255			
Lys	Ile	Ala	Leu	Pro	Lys	Glu	Tyr	Leu	Gly	Glu	Gly	Ile	Asp	Pro	Glu	
				260					265				270			
Val	Lys	Glu	Thr	Ile	Leu	Asn	Ala	Ala	Lys	His	Phe	Glu	Lys	Leu	Gly	
				275					280				285			
Ala	Ile	Val	Glu	Glu	Val	Ser	Leu	Pro	His	Ser	Lys	Tyr	Gly	Val	Ala	
				290					295				300			
Val	Tyr	Tyr	Ile	Ile	Ala	Ser	Ser	Glu	Ala	Ser	Ser	Asn	Leu	Gln	Arg	
				305					310				315			
Phe	Asp	Gly	Ile	Arg	Tyr	Gly	Tyr	Arg	Ala	Glu	Asp	Ala	Thr	Asn	Leu	
				325					330				335			
Asp	Glu	Ile	Tyr	Val	Asn	Ser	Arg	Ser	Gln	Gly	Phe	Gly	Glu	Glu	Val	
				340					345				350			
Lys	Arg	Arg	Ile	Met	Leu	Gly	Thr	Phe	Ser	Leu	Ser	Ser	Gly	Tyr	Tyr	
				355					360				365			
Asp	Ala	Tyr	Tyr	Lys	Lys	Ala	Gly	Gln	Val	Arg	Thr	Leu	Ile	Ile	Gln	
				370					375				380			
Asp	Phe	Glu	Lys	Val	Phe	Ala	Asp	Tyr	Asp	Leu	Ile	Leu	Gly	Pro	Thr	
				385					390				395			
Ala	Pro	Ser	Val	Ala	Tyr	Asp	Leu	Asp	Ser	Leu	Asn	His	Asp	Pro	Val	
				405					410				415			

Ala Met Tyr Leu Ala Asp Leu Leu Thr Ile Pro Val Asn Leu Ala Gly
 420 425 430

Leu Pro Gly Ile Ser Ile Pro Ala Gly Phe Ser Gln Gly Leu Pro Val
 435 440 445

Gly Leu Gln Leu Ile Gly Pro Lys Tyr Ser Glu Glu Thr Ile Tyr Gln
 450 455 460

Ala Ala Ala Ala Phe Glu Ala Thr Thr Asp Tyr His Lys Gln Gln Pro
 465 470 475 480

Val Ile Phe Gly Gly Asp Asn
 485

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTTACAGGT AAACAACACTAC AAGTCGGCGA CAAGGCGCTT GATTTTTCTC TTACTACAAC 60

AGATCTTTCT AAAAAATCTC TGGCTGATTT TGATGGCAAG AAAAAAGTCT TGAGTGTCGT 120

TCCTTCTATC GATACAGGCA TCTGCTCAAC TCAAACACGT CGTTTTAATG AAGAATTGGC 180

TGGACTGGAC AACACGGTCG TATTGACTGT TTCAATGGAC CTACCTTTTG CTCAAAAACG 240

TTGGTGCGGT GCTGAAGGCC TTGACAATGC CATTATGCTT TCAGACTACT TTGACCATTG 300

TTTCGGGCGC GATTATGCCC TCTTGATCAA CGAATGGCAC CTATTAGCAC GCGCAGTCTT 360

TGTCCTCGAT ACTGACAATA CGATTGCTA CGTTGAATAC GTGGATAATA TCAATTCTGA 420

GCCAAACTTC GAA 433

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Thr Gly Lys Gln Leu Gln Val Gly Asp Lys Ala Leu Asp Phe Ser
 1 5 10 15

Leu Thr Thr Thr Asp Leu Ser Lys Lys Ser Leu Ala Asp Phe Asp Gly
 20 25 30

Lys Lys Lys Val Leu Ser Val Val Pro Ser Ile Asp Thr Gly Ile Cys

35	40	45
Ser Thr Gln Thr Arg Arg Phe Asn Glu Glu Leu Ala Gly Leu Asp Asn		
50	55	60
Thr Val Val Leu Thr Val Ser Met Asp Leu Pro Phe Ala Gln Lys Arg		
65	70	75
Trp Cys Gly Ala Glu Gly Leu Asp Asn Ala Ile Met Leu Ser Asp Tyr		
85	90	95
Phe Asp His Ser Phe Gly Arg Asp Tyr Ala Leu Leu Ile Asn Glu Trp		
100	105	110
His Leu Leu Ala Arg Ala Val Phe Val Leu Asp Thr Asp Asn Thr Ile		
115	120	125
Arg Tyr Val Glu Tyr Val Asp Asn Ile Asn Ser Glu Pro Asn Phe Glu		
130	135	140

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CCAGGCTGAT ACAAGTATCG CAGACATTCA AAAAAGAGGC GAACTGGTTG TCGGTGTCAA	60
ACAAGACGTT CCCAATTTTG GTTACAAnGA TCCCAAGACC GGTACTTATT CTGGTATCGA	120
AaCCGACTTG GCCAAGATGG TAGCTGATGA ACTCAAGGTC AAGATTCGCT ATGTGCCGGT	180
TACAGCACAA ACCCGCGGCC CCCTTCTAGA CAATGAACAG GTCGATATGG ATATCGCGAC	240
CTTTACCATC ACGGACGAAC GCAAAAAACT CTACAACTTT ACCAGTCCCT ACTACACAGA	300
CGCTTCTGGA TTTTGGTCA ATAAATCTGC CAAAATCAAA AAGATTGAGG ACCTAAACGG	360
CAAAACCATC GGAGTCGCCC AAGGTTCTAT CACCCAACGC CTGATTACTG AACTGGGTAA	420
AAAGAAAGGT CTGAAGTTTA AATTCGTCTGA ACTTGGTTCC TACCCAGAAT TGATTACTTC	480
CCTGCACGCT CATCGTATCG ATACCTTTTC CGTTGACCGC TCTATTCTAT CTGGCTACAC	540
TAGTAAACGG ACAGCACTAC TAGATGATAG TTTCAAGCCA TCTGACTACG GTATTGTTAC	600
CAAGAAATCA AATACAGAGC TCAACGACTA TCTTGATAAC TTGGTTACTA AATGGAGCAA	660
GGATGGTAGT TTGCAGAAAC TTTATGACCG TTACAAGCTC AAACCATCTA GCCATACTGC	720
AGAT	724

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gln Ala Asp Thr Ser Ile Ala Asp Ile Gln Lys Arg Gly Glu Leu Val
 1 5 10 15
 Val Gly Val Lys Gln Asp Val Pro Asn Phe Gly Tyr Xaa Asp Pro Lys
 20 25 30
 Thr Gly Thr Tyr Ser Gly Ile Glu Thr Asp Leu Ala Lys Met Val Ala
 35 40 45
 Asp Glu Leu Lys Val Lys Ile Arg Tyr Val Pro Val Thr Ala Gln Thr
 50 55 60
 Arg Gly Pro Leu Leu Asp Asn Glu Gln Val Asp Met Asp Ile Ala Thr
 65 70 75 80
 Phe Thr Ile Thr Asp Glu Arg Lys Lys Leu Tyr Asn Phe Thr Ser Pro
 85 90 95
 Tyr Tyr Thr Asp Ala Ser Gly Phe Leu Val Asn Lys Ser Ala Lys Ile
 100 105 110
 Lys Lys Ile Glu Asp Leu Asn Gly Lys Thr Ile Gly Val Ala Gln Gly
 115 120 125
 Ser Ile Thr Gln Arg Leu Ile Thr Glu Leu Gly Lys Lys Lys Gly Leu
 130 135 140
 Lys Phe Lys Phe Val Glu Leu Gly Ser Tyr Pro Glu Leu Ile Thr Ser
 145 150 155 160
 Leu His Ala His Arg Ile Asp Thr Phe Ser Val Asp Arg Ser Ile Leu
 165 170 175
 Ser Gly Tyr Thr Ser Lys Arg Thr Ala Leu Leu Asp Asp Ser Phe Lys
 180 185 190
 Pro Ser Asp Tyr Gly Ile Val Thr Lys Lys Ser Asn Thr Glu Leu Asn
 195 200 205
 Asp Tyr Leu Asp Asn Leu Val Thr Lys Trp Ser Lys Asp Gly Ser Leu
 210 215 220
 Gln Lys Leu Tyr Asp Arg Tyr Lys Leu Lys Pro Ser Ser His Thr Ala
 225 230 235 240
 Asp

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTCTGTATCA TTTGAAAACA AAGAAACAAA CCGTGGTGTC TTgACTTTCA CTATCTCTCA 60
 AGACCAAATC AAACCAGAAT TGGACCGTGT CTTCAAGtCA GTGAAGAAAT CTCTTAATGT 120
 TCCAGGTTTC CGTAAAGGTC ACCTTCCACG CCCTATCTTC GACCAAAAAT TTGGTGAAGA 180
 AGCTCTTTAT CAAGATGCAA TGAACGCACT TTTGCCAAAC GCTTATGAAG CAGCTGTAAA 240
 AGAAGCTGGT CTTGAAGTGG TTGCCCAACC AAAAATTGAC GTAACCTCAA TGGAAAAGG 300
 TCAAGACTGG GTTATCACTG CTGAAGTCGT TACAAAACCT GAAGTAAAAT TGGGTGACTA 360
 CAAAAACCTT GAAGTATCAG TTGATGTAGA AAAAGAAGTA ACTGACGCTG ATGTCGAAGA 420
 GCGTATCGAA CGCGAACGCA ACAACCTGGC TGAATTGGTT ATCAAGGAAG CTGCTGCTGA 480
 AAACGGCGAC ACTGTTGTGA TCGACTTCGT TGGTTCATC GACGGTGTG AATTTGACGG 540
 TGGAAAAGGT GAAAACCTCT CACTTGGACT TGGTTCAGGT CAATTCATCC CTGGTTTCGA 600
 AGACCAATTG GTAGGTCACT CAGCTGGCGA AACCGTTGAT GTTATCGTAA CATTCCCAGA 660
 AGACTACCAA GCAGAAGACC TTGCAGGTAA AGAAGCTAAA TTCGTGACAA CTATCCACGA 720
 AGTAAAAGCT AAAGAAGTTC CGGCTCTTGA CGATGAACTT GCAAAAGACA TTGATGAAGA 780
 AGTTGAAACA CTTGCTGACT TGAAAGAAAA ATACAGCAAA GAATTGGCTG CTGCTAAAGA 840
 AGAAGCTTAC AAAGATGCAG TTGAAGGTGC AGCAATTGAT ACAGCTGTAG AAAATGCTGA 900
 AATCGTAGAA CTTCCAGAAG AAATGATCCA TGAAGAAGTT CACCGTTCAG TAAATGAATT 960
 CCTTGGGAAT TTGCAACGTC AAGGGATCAA CCCTGACATG TACTTCCAAA TCACTGGAAC 1020
 TACTCAAGAA GACCTTCACA ACCAATACCA AGCAGAAGCT GAGTCACGTA CTAAGACTAA 1080
 CCTTGTTATC GAAGCAGTTG CCAAAGCTGA AGGATTTGAT GCTTCAGAAG AAGAAATCCA 1140
 AAAAGAAGTT GAGCAATTGG CAGCAGACTA CAACATGGAA GTTGCACAAG TTCAAAACTT 1200
 GCTTTCAGCT GACATGTTGA AACATGATAT CACTATCAAA AAAGCTGTTG AATTGATCAC 1260
 AAGCACAGCA ACAGTAAAA 1279

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Val Ser Phe Glu Asn Lys Glu Thr Asn Arg Gly Val Leu Thr Phe

1					5					10					15				
Thr	Ile	Ser	Gln	Asp	Gln	Ile	Lys	Pro	Glu	Leu	Asp	Arg	Val	Phe	Lys				
			20					25					30						
Ser	Val	Lys	Lys	Ser	Leu	Asn	Val	Pro	Gly	Phe	Arg	Lys	Gly	His	Leu				
		35					40					45							
Pro	Arg	Pro	Ile	Phe	Asp	Gln	Lys	Phe	Gly	Glu	Glu	Ala	Leu	Tyr	Gln				
	50					55					60								
Asp	Ala	Met	Asn	Ala	Leu	Leu	Pro	Asn	Ala	Tyr	Glu	Ala	Ala	Val	Lys				
65					70					75					80				
Glu	Ala	Gly	Leu	Glu	Val	Val	Ala	Gln	Pro	Lys	Ile	Asp	Val	Thr	Ser				
				85					90					95					
Met	Glu	Lys	Gly	Gln	Asp	Trp	Val	Ile	Thr	Ala	Glu	Val	Val	Thr	Lys				
			100					105					110						
Pro	Glu	Val	Lys	Leu	Gly	Asp	Tyr	Lys	Asn	Leu	Glu	Val	Ser	Val	Asp				
		115					120					125							
Val	Glu	Lys	Glu	Val	Thr	Asp	Ala	Asp	Val	Glu	Glu	Arg	Ile	Glu	Arg				
	130					135					140								
Glu	Arg	Asn	Asn	Leu	Ala	Glu	Leu	Val	Ile	Lys	Glu	Ala	Ala	Ala	Glu				
145					150					155					160				
Asn	Gly	Asp	Thr	Val	Val	Ile	Asp	Phe	Val	Gly	Ser	Ile	Asp	Gly	Val				
				165					170					175					
Glu	Phe	Asp	Gly	Gly	Lys	Gly	Glu	Asn	Phe	Ser	Leu	Gly	Leu	Gly	Ser				
			180					185					190						
Gly	Gln	Phe	Ile	Pro	Gly	Phe	Glu	Asp	Gln	Leu	Val	Gly	His	Ser	Ala				
		195					200					205							
Gly	Glu	Thr	Val	Asp	Val	Ile	Val	Thr	Phe	Pro	Glu	Asp	Tyr	Gln	Ala				
	210					215					220								
Glu	Asp	Leu	Ala	Gly	Lys	Glu	Ala	Lys	Phe	Val	Thr	Thr	Ile	His	Glu				
225					230					235					240				
Val	Lys	Ala	Lys	Glu	Val	Pro	Ala	Leu	Asp	Asp	Glu	Leu	Ala	Lys	Asp				
				245					250					255					
Ile	Asp	Glu	Glu	Val	Glu	Thr	Leu	Ala	Asp	Leu	Lys	Glu	Lys	Tyr	Ser				
			260					265					270						
Lys	Glu	Leu	Ala	Ala	Ala	Lys	Glu	Glu	Ala	Tyr	Lys	Asp	Ala	Val	Glu				
		275					280					285							
Gly	Ala	Ala	Ile	Asp	Thr	Ala	Val	Glu	Asn	Ala	Glu	Ile	Val	Glu	Leu				
	290					295					300								
Pro	Glu	Glu	Met	Ile	His	Glu	Glu	Val	His	Arg	Ser	Val	Asn	Glu	Phe				
305					310					315					320				
Leu	Gly	Asn	Leu	Gln	Arg	Gln	Gly	Ile	Asn	Pro	Asp	Met	Tyr	Phe	Gln				
				325					330					335					
Ile	Thr	Gly	Thr																

159

340

345

350

Ala Glu Ser Arg Thr Lys Thr Asn Leu Val Ile Glu Ala Val Ala Lys
355 360 365

Ala Glu Gly Phe Asp Ala Ser Glu Glu Glu Ile Gln Lys Glu Val Glu
370 375 380

Gln Leu Ala Ala Asp Tyr Asn Met Glu Val Ala Gln Val Gln Asn Leu
385 390 395 400

Leu Ser Ala Asp Met Leu Lys His Asp Ile Thr Ile Lys Lys Ala Val
405 410 415

Glu Leu Ile Thr Ser Thr Ala Thr Val Lys
420 425

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

TGGTCAAAG GAAAGTCAGA CAGGAAAGGG GATGAAAATT GTGACCAGTT TTTATCCTAT	60
CTACGCTATG GTTAAGGAAG TATCTGGTGA CTTGAATGAT GTTCGGATGA TTCAGTCAAG	120
TAGTGGTATT CACTCCTTTG AACCTTCGGC AAATGATATC GCAGCCATCT ATGATGCAGA	180
TGTCTTTGTT TACCATTCTC ATACACTCGA ATCTTGGGCA GGAAGTCTGG ATCCAAATCT	240
AAAAAAATCC AAAGTGAAGG TCTTAGAGGC TTCTGAGGGA ATGACCTTGG AACGTGTCCC	300
TGGACTAGAG GATGTGGAAG CAGGGGATGG AGTTGATGAA AAAACGCTCT ATGACCCTCA	360
CACATGGCTA GATCCTGAAA AAGCTGGAGA AGAAGCCCAA ATTATCGCTG ATAAACTTTC	420
AGAGGTGGAT AGTGAGCATA AAGAGACTTA TCAAAAAAAT GCGCAACCTT TATCAAAAAA	480
GCTCAGGAAT	490

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Gln Lys Glu Ser Gln Thr Gly Lys Gly Met Lys Ile Val Thr Ser
1 - 5 10 15

160

Phe Tyr Pro Ile Tyr Ala Met Val Lys Glu Val Ser Gly Asp Leu Asn
 20 25 30
 Asp Val Arg Met Ile Gln Ser Ser Ser Gly Ile His Ser Phe Glu Pro
 35 40 45
 Ser Ala Asn Asp Ile Ala Ala Ile Tyr Asp Ala Asp Val Phe Val Tyr
 50 55 60
 His Ser His Thr Leu Glu Ser Trp Ala Gly Ser Leu Asp Pro Asn Leu
 65 70 75 80
 Lys Lys Ser Lys Val Lys Val Leu Glu Ala Ser Glu Gly Met Thr Leu
 85 90 95
 Glu Arg Val Pro Gly Leu Glu Asp Val Glu Ala Gly Asp Gly Val Asp
 100 105 110
 Glu Lys Thr Leu Tyr Asp Pro His Thr Trp Leu Asp Pro Glu Lys Ala
 115 120 125
 Gly Glu Glu Ala Gln Ile Ile Ala Asp Lys Leu Ser Glu Val Asp Ser
 130 135 140
 Glu His Lys Glu Thr Tyr Gln Lys Asn Ala Gln Pro Leu Ser Lys Lys
 145 150 155 160
 Leu Arg Asn

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAAGGATAGA TATATTTTAG CATTTGAGAC ATCCTGTGAT GAGACCAGTG TCGCCGTCTT	60
GAAAAACGAC GATGAGCTCT TGTCCAATGT CATTGCTAGT CAAATTGAGA GTCACAAACG	120
TTTTGGTGGC GTAGTGCCCG AAGTAGCCAG TCGTCACCAT GTCGAGGTCA TTACAGCCTG	180
TATCGAGGAG GCATTGGCAG AAGCAGGGAT TACCGAAGAG GACGTGACAG CTGTTGCGGT	240
TACCTACGGA CCAGGCTTGG TCGGAGCCTT GCTAGTTGGT TTGTCAGCTG CCAAGGCCTT	300
TGCTTGGGCT CACGGACTTC CACTGATTCC TGTTAATCAC ATGGCTGGGC ACCTCATGGC	360
AGCTCAGAGT GTGGAGCCTT TGGAGTTTCC CTTGCTAGCC CTCTTGGTCA GCGGCGGACA	420
CACAGAGTTG GTTTATGTTT CGGAGGCAGG AGATTATAAG ATTGTTGGGG AAACCCGTGA	480
TGATGCGGTT GGTGAGGCTT ATGATAAGGT CGGCCGTGTC ATGGGCTTGA CCTATCCTGC	540
AGGTCGTGAG ATTGACGAGC TGGCTCATCA GGGGCAGGAT ATTTATGATT TCCCCCGTGC	600
CATGATTAAG GAAGATAATC TGGAGTTCTC CTTCTCAGGT TTGAAATCTG CCTTTATCAA	660

TCTTCATCAC AATGCCGAGC AAAAGGGAGA AAGCCTGTCT ACAGAAGATT TGTGTGCTTC 720
 CTTCCAAGCA GCAGTTATGG ACATTCTCAT GGCAAAACC AAGAAGGCTT TGGAGAAATA 780
 TCCTGTTAAA ATCCTAGTTG TGGCAGGTGG TGTGGCAGCC AATAAAGGTC TCAGAGAACG 840
 CCTAGCAGCC GAAATCACAG ATGTCAAGGT TATCATCCCC CCTCTGCGAC TCTGCGGAGA 900
 CAATGCAGGT ATGATTGCCT ATGCCAGCGT CAGCNA GTGG AACAAAGAAA ACTTCGCAGG 960
 CTGGGACCTC AATGCCAAAC CAAGTCTTGC CTTTGATACC ATGGAA 1006

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Lys Asp Arg Tyr Ile Leu Ala Phe Glu Thr Ser Cys Asp Glu Thr Ser
 1 5 10 15
 Val Ala Val Leu Lys Asn Asp Asp Glu Leu Leu Ser Asn Val Ile Ala
 20 25 30
 Ser Gln Ile Glu Ser His Lys Arg Phe Gly Gly Val Val Pro Glu Val
 35 40 45
 Ala Ser Arg His His Val Glu Val Ile Thr Ala Cys Ile Glu Glu Ala
 50 55 60
 Leu Ala Glu Ala Gly Ile Thr Glu Glu Asp Val Thr Ala Val Ala Val
 65 70 75 80
 Thr Tyr Gly Pro Gly Leu Val Gly Ala Leu Leu Val Gly Leu Ser Ala
 85 90 95
 Ala Lys Ala Phe Ala Trp Ala His Gly Leu Pro Leu Ile Pro Val Asn
 100 105 110
 His Met Ala Gly His Leu Met Ala Ala Gln Ser Val Glu Pro Leu Glu
 115 120 125
 Phe Pro Leu Leu Ala Leu Leu Val Ser Gly Gly His Thr Glu Leu Val
 130 135 140
 Tyr Val Ser Glu Ala Gly Asp Tyr Lys Ile Val Gly Glu Thr Arg Asp
 145 150 155 160
 Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Gly Arg Val Met Gly Leu
 165 170 175
 Thr Tyr Pro Ala Gly Arg Glu Ile Asp Glu Leu Ala His Gln Gly Gln
 180 185 190
 Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile Lys Glu Asp Asn Leu Glu

195	200	205
Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe Ile Asn Leu His His Asn		
210	215	220
Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr Glu Asp Leu Cys Ala Ser		
225	230	235 240
Phe Gln Ala Ala Val Met Asp Ile Leu Met Ala Lys Thr Lys Lys Ala		
	245	250 255
Leu Glu Lys Tyr Pro Val Lys Ile Leu Val Val Ala Gly Gly Val Ala		
	260	265 270
Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala Ala Glu Ile Thr Asp Val		
	275	280 285
Lys Val Ile Ile Pro Pro Leu Arg Leu Cys Gly Asp Asn Ala Gly Met		
	290	295 300
Ile Ala Tyr Ala Ser Val Ser Xaa Trp Asn Lys Glu Asn Phe Ala Gly		
305	310	315 320
Trp Asp Leu Asn Ala Lys Pro Ser Leu Ala Phe Asp Thr Met Glu		
	325	330 335

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGTAGTTAAA GTTGGTATTA ACGGTTTCGG ACGTATCGGT CGTCTTGCTT TCCGTCGTAT	60
CCAAAACGTA GAAGGTGTTG AAGTTACACG CATCAACGAC CTTACAGATC CAGTTATGCT	120
TGCACACTTG TTGAAATACG ACACAACCTCA AGGTCGTTTC GACGGTACTG TTGAAGTTAA	180
AGAAGGTGGA TTTGAAGTTA ACGGTAAATT CATCAAAGTT TCTGCTGAAC GTGATCCAGA	240
ACAAATCGAC TGGGCTACTG ACGGTGTAGA AATCGTTCTT GAAGCTACTG GTTCTTTTGC	300
TAAGAAAGAA GCAGCTGAAA AACACCTTAA AGGTGGAGCT AAAAAAGTTG TTATCACTGC	360
TCCTGGTGGA AACGACGTTA AAACAGTTGT ATTCAACACT AACCACGACG TTCTTGACGG	420
TACTGAAACA GTTATCTCAG GTGCTTCATG TACTACAAAC TGCTTGGCTC CAATGGCTAA	480
AGCTCTTCAA GACAACTTTG GTGTTGTTGA AGGATTGATG ACTACTATCC ACGCTTACAC	540
TGGTGACCAA ATGATCCTTG ACGGACCACA CCGTGGTGGT GACCTTCGCC GTGCTCGCGC	600
TGGTGCTGCA AACATCGTTC CTAACCTAAC TGGTGCTGCA AAAGCTATCG GTCTTGTAAT	660
CCCAGAATTG AATGGTAAAC TTGACGGATC TGCACAACGC GTTCCAACCT CAACTGGATC	720
AGTTACTGAA TTGGTAGCAG TTCTTGAAAA GAACGTTACT GTTGATGAAG TGAACGCAGC	780

(2) INFORMATION FOR SEO ID NO:54:

(A) LENGTH: 333 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:54:

Val	Val	Lys	Val	Gly	Ile	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Leu	Ala
1				5					10					15	
Phe	Arg	Arg	Ile	Gln	Asn	Val	Glu	Gly	Val	Glu	Val	Thr	Arg	Ile	Asn
			20					25					30		
Asp	Leu	Thr	Asp	Pro	Val	Met	Leu	Ala	His	Leu	Leu	Lys	Tyr	Asp	Thr
		35					40					45			
Thr	Gln	Gly	Arg	Phe	Asp	Gly	Thr	Val	Glu	Val	Lys	Glu	Gly	Gly	Phe
	50					55					60				
Glu	Val	Asn	Gly	Lys	Phe	Ile	Lys	Val	Ser	Ala	Glu	Arg	Asp	Pro	Glu
65					70					75					80
Gln	Ile	Asp	Trp	Ala	Thr	Asp	Gly	Val	Glu	Ile	Val	Leu	Glu	Ala	Thr
				85					90					95	
Gly	Phe	Phe	Ala	Lys	Lys	Glu	Ala	Ala	Glu	Lys	His	Leu	Lys	Gly	Gly
			100					105					110		
Ala	Lys	Lys	Val	Val	Ile	Thr	Ala	Pro	Gly	Gly	Asn	Asp	Val	Lys	Thr
		115					120					125			
Val	Val	Phe	Asn	Thr	Asn	His	Asp	Val	Leu	Asp	Gly	Thr	Glu	Thr	Val
	130					135						140			
Ile	Ser	Gly	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Met	Ala	Lys
145					150					155					160
Ala	Leu	Gln	Asp	Asn	Phe	Gly	Val	Val	Glu	Gly	Leu	Met	Thr	Thr	Ile
				165					170					175	
His	Ala	Tyr	Thr	Gly	Asp	Gln	Met	Ile	Leu	Asp	Gly	Pro	His	Arg	Gly
		180						185					190		
Gly	Asp	Leu	Arg	Arg	Ala	Arg	Ala	Gly	Ala	Ala	Asn	Ile	Val	Pro	Asn
		195					200					205			
Ser	Thr	Gly	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Val	Ile	Pro	Glu	Leu	Asn
	210					215						220			

Gly Lys Leu Asp Gly Ser Ala Gln Arg Val Pro Thr Pro Thr Gly Ser
 225 230 235 240
 Val Thr Glu Leu Val Ala Val Leu Glu Lys Asn Val Thr Val Asp Glu
 245 250 255
 Val Asn Ala Ala Met Lys Ala Ala Ser Asn Glu Ser Tyr Gly Tyr Thr
 260 265 270
 Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Tyr Gly Ser
 275 280 285
 Leu Phe Asp Ala Thr Gln Thr Lys Val Leu Asp Val Asp Gly Lys Gln
 290 295 300
 Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr Ala
 305 310 315 320
 Gln Leu Val Arg Thr Leu Gly Ile Leu Arg Lys Asn Cys
 325 330

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TTCTTACGAG TTGGGACTGT ATCAAGCTAG AACGGTTAAG GAAAATAATC GTGTTTCCTA	60
TATAGATGGA AAACAAGCGA CGCAAAAAAC GGAGAATTG ACTCCTGATG AGGTTAGCAA	120
GCGTGAAGGA ATCAATGCTG AGCAAATCGT CATCAAGATA ACAGACCAAG GCTATGTCAC	180
TTCACATGGC GACCACTATC ATTATTACAA TGGAAGGTT CTTTATGACG CTATCATCAG	240
TGAAGAATTA CTCATGAAAG ATCCAAACTA TAAGCTAAAA GATGAGGATA TTGTTAATGA	300
GGTCAAGGGT GGATATGTTA TCAAGGTAGA TGGAAAATAC TATGTTTACC TTAAGGATGC	360
TGCCCACGCG GATAACGTCC GTACAAAAGA GGAAATCAAT CGACAAAAAC AAGAGCATAG	420
TCAACATCGT GAAGGTGGAA CTCCAAGAAA CGATGGTGCT GTTGCCTTGG CACGTTTCGA	480
AGGACGCTAT ACTACAGATG ATGGTTATAT CTTTAATGCT TCTGATATCA TAGAGGATAC	540
TGGTGATGCT TATATCGTTC CTCATGGAGA TCATTACCAT TACATTCCTA AGAATGAGTT	600
ATCAGCTAGC GAGTTGGCTG CTGCAGAAGC CTTCTATCT GGTGAGGAA ATCTGTCAAA	660
TTCAAGAACC TATCGCCGAC AAAATAGCGA TAACACTTCA AGAACAACT GGGTACCTTC	720
TGTAAGCAAT CCAGGAATA CAAATACTAA CACAAGCAAC AACAGCAACA CTAACAGTCA	780
AGCAAGTCAA AGTAATGACA TTGATAGTCT CTTGAAACAG CTCTACAAAC TGCCTTTGAG	840
TCAACGACAT GTAGAATCTG ATGGCCTTGT CTTTGATCCA GCACAAATCA CAAGTCGAAC	900
AGCTAGAGGT GTTGCAGTGC CACACGGAGA TCATTACCAC TTCATCCCTT ACTCTCAAT	960

GTCTGAATTG GAAGAACGAA TCGCTCGTAT TATTCCCCTT CGTTATCGTT CAAACCATTG 1020
 GGTACCAGAT TCAAGGCCAG AACAACCAAG TCCACAACCG ACTCCGGAAC CTAGTCCAGG 1080
 CCCGCAACCT GCACCAAATC TTAAATAGA CTCAAATTCT TCTTTGGTTA GTCAGCTGGT 1140
 ACGAAAAGTT GGGGAAGGAT ATGTATTCTGA AGAAAAGGGC ATCTCTCGTT ATGTCTTTGC 1200
 GAAAGATTTA CCATCTGAAA CTGTTAAAAA TCTTGAAAGC AAGTTATCAA AACAAGAGAG 1260
 TGTTCACAC ACTTTAACTG CTAAAAAGA AAATGTTGCT CCTCGTGACC AAGAATTTTA 1320
 TGATAAGCA TATAATCTGT TAACTGAGGC TCATAAAGCC TTGTTTGNAA ATAAGGGTCG 1380
 TAATTCTGAT TTCCAAGCCT TAGACAAATT ATTAGAACGC TTGAATGATG AATCGACTAA 1440
 TAAAGAAAAA TTGGTAGATG ATTTATTGGC ATTCCTAGCA CCAATTACCC ATCCAGAGCG 1500
 ACTTGGCAAA CCAAATTCTC AAATTGAGTA TACTGAAGAC GAAGTTCGTA TTGCTCAATT 1560
 AGCTGATAAG TATACAACGT CAGATGGTTA CATTTTGTAT GAACATGATA TAATCAGTGA 1620
 TGAAGGAGAT GCATATGTAA CGCCTCATAT GGGCCATAGT CACTGGATTG GAAAAGATAG 1680
 CCTTTCTGAT AAGGAAAAAG TTGCAGCTCA AGCCTATACT AAAGAAAAAG GTATCCTACC 1740
 TCCATCTCCA GACGCAGATG TTAAAGCAAA TCCAAGTGA GATAGTGCAG CAGCTATTTA 1800
 CAATCGTGTG AAAGGGGAAA AACGAATTCC ACTCGTTCGA CTTCCATATA TGGTTGAGCA 1860
 TACAGTTGAG GTTAAAAACG GTAATTTGAT TATTCCTCAT AAGGATCATT ACCATAATAT 1920
 TAAATTTGCT TGGTTTGATG ATCACACATA CAAAGCTCCA AATGGCTATA CCTTGGAAGA 1980
 TTTGTTTGCG ACGATTAAAGT ACTACGTAGA ACACCTGAC GAACGTCCAC ATTCTAATGA 2040
 TGGATGGGGC AATGCCAGTG AGCATGTGTT AGGCAAGAAA GACCACAGTG AAGATCCAAA 2100
 TAAGAACTTC AAAGCGGATG AAGAGCCAGT AGAGGAAACA CCTGCTGAGC CAGAAGTCCC 2160
 TCAAGTAGAG ACTGAAAAAG TAGAAGCCCA ACTCAAAGAA GCAGAAGTTT TGCTTGCGAA 2220
 AGTAACGGAT TCTAGTCTGA AAGCCAATGC AACAGAAACT CTAGCTGGTT TACGAAATAA 2280
 TTTGACTCTT CAAATTATGG ATAACAATAG TATCATGGCA GAAGCAGAAA AATTACTTGC 2340
 GTTGTTAAAA GGAAGTAATC CTTATCTGT AAGTAAGGAA AAAATAAAC 2389

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 796 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Tyr Glu Leu Gly Leu Tyr Gln Ala Arg Thr Val Lys Glu Asn Asn

1	5					10					15				
Arg	Val	Ser	Tyr	Ile	Asp	Gly	Lys	Gln	Ala	Thr	Gln	Lys	Thr	Glu	Asn
			20					25					30		
Leu	Thr	Pro	Asp	Glu	Val	Ser	Lys	Arg	Glu	Gly	Ile	Asn	Ala	Glu	Gln
		35					40					45			
Ile	Val	Ile	Lys	Ile	Thr	Asp	Gln	Gly	Tyr	Val	Thr	Ser	His	Gly	Asp
	50					55					60				
His	Tyr	His	Tyr	Tyr	Asn	Gly	Lys	Val	Pro	Tyr	Asp	Ala	Ile	Ile	Ser
65					70					75					80
Glu	Glu	Leu	Leu	Met	Lys	Asp	Pro	Asn	Tyr	Lys	Leu	Lys	Asp	Glu	Asp
				85					90					95	
Ile	Val	Asn	Glu	Val	Lys	Gly	Gly	Tyr	Val	Ile	Lys	Val	Asp	Gly	Lys
			100					105					110		
Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala	Asp	Asn	Val	Arg	Thr
		115					120					125			
Lys	Glu	Glu	Ile	Asn	Arg	Gln	Lys	Gln	Glu	His	Ser	Gln	His	Arg	Glu
	130					135					140				
Gly	Gly	Thr	Pro	Arg	Asn	Asp	Gly	Ala	Val	Ala	Leu	Ala	Arg	Ser	Gln
145					150					155					160
Gly	Arg	Tyr	Thr	Thr	Asp	Asp	Gly	Tyr	Ile	Phe	Asn	Ala	Ser	Asp	Ile
				165					170					175	
Ile	Glu	Asp	Thr	Gly	Asp	Ala	Tyr	Ile	Val	Pro	His	Gly	Asp	His	Tyr
			180					185					190		
His	Tyr	Ile	Pro	Lys	Asn	Glu	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala
		195					200					205			
Glu	Ala	Phe	Leu	Ser	Gly	Arg	Gly	Asn	Leu	Ser	Asn	Ser	Arg	Thr	Tyr
	210					215					220				
Arg	Arg	Gln	Asn	Ser	Asp	Asn	Thr	Ser	Arg	Thr	Asn	Trp	Val	Pro	Ser
225					230					235					240
Val	Ser	Asn	Pro	Gly	Thr	Thr	Asn	Thr	Asn	Thr	Ser	Asn	Asn	Ser	Asn
				245					250					255	
Thr	Asn	Ser	Gln	Ala	Ser	Gln	Ser	Asn	Asp	Ile	Asp	Ser	Leu	Leu	Lys
			260					265					270		
Gln	Leu	Tyr	Lys	Leu	Pro	Leu	Ser	Gln	Arg	His	Val	Glu	Ser	Asp	Gly
		275					280					285			
Leu	Val	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr	Ala	Arg	Gly	Val
	290					295					300				
Ala	Val	Pro	His	Gly	Asp	His	Tyr	His	Phe	Ile	Pro	Tyr	Ser	Gln	Met
305					310					315					320
Ser	Glu	Leu	Glu	Glu	Arg	Ile	Ala	Arg	Ile	Ile	Pro	Leu	Arg	Tyr	Arg
				325					330					335	
Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Gln	Pro	Ser	Pro	Gln

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Pro Thr Pro Glu Pro Ser Pro Gly Pro Gln Pro Ala Pro Asn Leu Lys
355 360 365

Ile Asp Ser Asn Ser Ser Leu Val Ser Gln Leu Val Arg Lys Val Gly
370 375 380

Glu Gly Tyr Val Phe Glu Glu Lys Gly Ile Ser Arg Tyr Val Phe Ala
385 390 395 400

Lys Asp Leu Pro Ser Glu Thr Val Lys Asn Leu Glu Ser Lys Leu Ser
405 410 415

Lys Gln Glu Ser Val Ser His Thr Leu Thr Ala Lys Lys Glu Asn Val
420 425 430

Ala Pro Arg Asp Gln Glu Phe Tyr Asp Lys Ala Tyr Asn Leu Leu Thr
435 440 445

Glu Ala His Lys Ala Leu Phe Xaa Asn Lys Gly Arg Asn Ser Asp Phe
450 455 460

Gln Ala Leu Asp Lys Leu Leu Glu Arg Leu Asn Asp Glu Ser Thr Asn
465 470 475 480

Lys Glu Lys Leu Val Asp Asp Leu Leu Ala Phe Leu Ala Pro Ile Thr
485 490 495

His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile Glu Tyr Thr Glu
500 505 510

Asp Glu Val Arg Ile Ala Gln Leu Ala Asp Lys Tyr Thr Thr Ser Asp
515 520 525

Gly Tyr Ile Phe Asp Glu His Asp Ile Ile Ser Asp Glu Gly Asp Ala
530 535 540

Tyr Val Thr Pro His Met Gly His Ser His Trp Ile Gly Lys Asp Ser
545 550 555 560

Leu Ser Asp Lys Glu Lys Val Ala Ala Gln Ala Tyr Thr Lys Glu Lys
565 570 575

Gly Ile Leu Pro Pro Ser Pro Asp Ala Asp Val Lys Ala Asn Pro Thr
580 585 590

Gly Asp Ser Ala Ala Ala Ile Tyr Asn Arg Val Lys Gly Glu Lys Arg
595 600 605

Ile Pro Leu Val Arg Leu Pro Tyr Met Val Glu His Thr Val Glu Val
610 615 620

Lys Asn Gly Asn Leu Ile Ile Pro His Lys Asp His Tyr His Asn Ile
625 630 635 640

Lys Phe Ala Trp Phe Asp Asp His Thr Tyr Lys Ala Pro Asn Gly Tyr
645 650 655

Thr Leu Glu Asp Leu Phe Ala Thr Ile Lys Tyr Tyr Val Glu His Pro
660 665 670

Asp Glu Arg Pro His Ser Asn Asp Gly Trp Gly Asn Ala Ser Glu His

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675	680	685
Val Leu Gly Lys Lys Asp His Ser Glu Asp Pro Asn Lys Asn Phe Lys		
690	695	700
Ala Asp Glu Glu Pro Val Glu Glu Thr Pro Ala Glu Pro Glu Val Pro		
705	710	715 720
Gln Val Glu Thr Glu Lys Val Glu Ala Gln Leu Lys Glu Ala Glu Val		
	725	730 735
Leu Leu Ala Lys Val Thr Asp Ser Ser Leu Lys Ala Asn Ala Thr Glu		
	740	745 750
Thr Leu Ala Gly Leu Arg Asn Asn Leu Thr Leu Gln Ile Met Asp Asn		
	755	760 765
Asn Ser Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu Leu Lys Gly		
	770	775 780
Ser Asn Pro Ser Ser Val Ser Lys Glu Lys Ile Asn		
	785	790 795

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TACTGAGATG CATCATAATC TAGGAGCTGA AAAGCGTTCA GCAGTGGCTA CTACTATCGA	60
TAGTTTTAAG GAGCGAAGTC AAAAAGTCAG AGCACTATCT GATCCAAATG TGCCTTTTGT	120
TCCCTTCTTT GGCTCTAGTG AATGGCTTCG TTTTGACGGT GCTCATTCTG CGGTATTAGC	180
TGAGAAATAC AATCGTTCCT ACCGTCCTTA TCTTTTAGGA CAGGGGGGAG CTGCATCGCT	240
TAACCAATAT TTTGGAATGC AACAGATGTT ACCACAGCTG GAGAATAAAC AAGTTGTGTA	300
TGTTATCTCA CCTCAGTGGT TCAGTAAAAA TGGCTATGAT CCAGCAGCCT TCCAGCAGTA	360
TTTTAATGGA GACCAGTTGA CTAGTTTTCT GAAACATCAA TCTGGGGATC AGGCTAGTCA	420
ATATGCAGCG ACTCGCTTAC TGCAACAGTT CCCAAACGTA GCTATGAAGG ACCTGGTTCA	480
GAAGTTGGCA AGTAAAGAAG AATTGTCGAC AGCAGACAAT GAAATGATTG AATTATTGGC	540
TCGTTTTAAT GAACGCCAAG CTCCTTTTTT TGGTCAGTTT TCGGTTAGAG GCTATGTTAA	600
CTACGATAAG CATGTAGCTA AGTATTTAAA AATCTTGCCA GACCAGTTTT CTATCAGGC	660
AATAGAAGAT GTTGTCAAAG CAGATGCTGA AAAAAATACT TCCAATAATG AGATGGGAAT	720
GGAAAATTAT TTCTATAATG AGCAGATCAA GAAGGATTTG AAGAAATTAA AGGATTCTCA	780
GAAAAGCTTT ACCTATCTCA AGTCGCCAGA GTATAATGNN TTGCAGTTGG TTTTAACACA	840

GTTTTCTAAA TCTAAGGTAA ACCCGATTTT TATCATTTCCA CCTGTTAATA AAAAATGGAT 900
 GNACTATGCT GGTCTACGAG AGGATATGTA CCAACAAACG GTGCAGAAGA TTCGCTACCA 960
 GTTAGAAAGT CAAGGTTTTA CCAATATAGC AGATTTTCTT AAGGACGGCG GGGAGCCTTT 1020
 CTTTATGAAG GACACCATTC ACCTTGGTTG GTTGGGTTGG TTGGCTTTTG ACAAGGCAGT 1080
 TGATCCTTTC CTATCCAATC CCACACCAGC TCCGACTTAC CATCTGAATG AGCGCTTTTT 1140
 CAGCAAAGAT TGGGCGACTT ATGATGGAGA TGTCAAAGAA 1180

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Thr	Glu	Met	His	His	Asn	Leu	Gly	Ala	Glu	Lys	Arg	Ser	Ala	Val	Ala	1	5	10	15
Thr	Thr	Ile	Asp	Ser	Phe	Lys	Glu	Arg	Ser	Gln	Lys	Val	Arg	Ala	Leu	20	25	30	
Ser	Asp	Pro	Asn	Val	Arg	Phe	Val	Pro	Phe	Phe	Gly	Ser	Ser	Glu	Trp	35	40	45	
Leu	Arg	Phe	Asp	Gly	Ala	His	Ser	Ala	Val	Leu	Ala	Glu	Lys	Tyr	Asn	50	55	60	
Arg	Ser	Tyr	Arg	Pro	Tyr	Leu	Leu	Gly	Gln	Gly	Gly	Ala	Ala	Ser	Leu	65	70	75	80
Asn	Gln	Tyr	Phe	Gly	Met	Gln	Gln	Met	Leu	Pro	Gln	Leu	Glu	Asn	Lys	85	90	95	
Gln	Val	Val	Tyr	Val	Ile	Ser	Pro	Gln	Trp	Phe	Ser	Lys	Asn	Gly	Tyr	100	105	110	
Asp	Pro	Ala	Ala	Phe	Gln	Gln	Tyr	Phe	Asn	Gly	Asp	Gln	Leu	Thr	Ser	115	120	125	
Phe	Leu	Lys	His	Gln	Ser	Gly	Asp	Gln	Ala	Ser	Gln	Tyr	Ala	Ala	Thr	130	135	140	
Arg	Leu	Leu	Gln	Gln	Phe	Pro	Asn	Val	Ala	Met	Lys	Asp	Leu	Val	Gln	145	150	155	160
Lys	Leu	Ala	Ser	Lys	Glu	Glu	Leu	Ser	Thr	Ala	Asp	Asn	Glu	Met	Ile	165	170	175	
Glu	Leu	Leu	Ala	Arg	Phe	Asn	Glu	Arg	Gln	Ala	Ser	Phe	Phe	Gly	Gln	180	185	190	
Phe	Ser	Val	Arg	Gly	Tyr	Val	Asn	Tyr	Asp	Lys	His	Val	Ala	Lys	Tyr	195	200	205	

Leu Lys Ile Leu Pro Asp Gln Phe Ser Tyr Gln Ala Ile Glu Asp Val
 210 215 220
 Val Lys Ala Asp Ala Glu Lys Asn Thr Ser Asn Asn Glu Met Gly Met
 225 230 235 240
 Glu Asn Tyr Phe Tyr Asn Glu Gln Ile Lys Lys Asp Leu Lys Lys Leu
 245 250 255
 Lys Asp Ser Gln Lys Ser Phe Thr Tyr Leu Lys Ser Pro Glu Tyr Asn
 260 265 270
 Xaa Leu Gln Leu Val Leu Thr Gln Phe Ser Lys Ser Lys Val Asn Pro
 275 280 285
 Ile Phe Ile Ile Pro Pro Val Asn Lys Lys Trp Met Xaa Tyr Ala Gly
 290 295 300
 Leu Arg Glu Asp Met Tyr Gln Gln Thr Val Gln Lys Ile Arg Tyr Gln
 305 310 315 320
 Leu Glu Ser Gln Gly Phe Thr Asn Ile Ala Asp Phe Ser Lys Asp Gly
 325 330 335
 Gly Glu Pro Phe Phe Met Lys Asp Thr Ile His Leu Gly Trp Leu Gly
 340 345 350
 Trp Leu Ala Phe Asp Lys Ala Val Asp Pro Phe Leu Ser Asn Pro Thr
 355 360 365
 Pro Ala Pro Thr Tyr His Leu Asn Glu Arg Phe Phe Ser Lys Asp Trp
 370 375 380
 Ala Thr Tyr Asp Gly Asp Val Lys Glu
 385 390

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTTTTGAGA AAGTATTTGC AGGGGGCCCT GATTGAGTCG ATTGAGCAAG TGGAAAATGA	60
CCGTATTGTG GAAATTACAG TTTCCAATAA AAACGAGATT GGAGACCATA TCCAGGCTAC	120
CTTGATTATC GAAATTATGG GGAAACACAG TAATATTCTA CTGGTCGATA AAAGCAGTCA	180
TAAAATCCTC GAAGTTATCA AACACGTCGG CTTTTACAA AATAGCTACC GCACCTTACT	240
TCCAGGATCG ACCTATATCG CTCCGCCAAG TACAAAATCT CTCAATCCTT TTACTATCAA	300
GGATGAAAAG CTCTTTGAAA TCCTGCAAAC CCAAGAACTA ACAGCAAAAA ATCTTCAAAG	360
CCTCTTTCAA GGTCTGGGAC GCGATACGGC AAATGAATTG GAAAGGATAC TGGTTAGTGA	420

AAAA CTTTCC GCTTTCCGAA ATTTTTTCAA TCAAGAAACC AAGCCATGCT TGACTGAGAC 480
 TTCCTTCAGT CCAGTTCCTT TTGCAAATCA GGTGGGAGAG CCTTTTGCAA ATCTTTCTGA 540
 TTTGTTGGAC ACCTACTATA AGGATAAGGC TGAGCGCGAC CGCGTCAAAC AGCAGGCCAG 600
 TGAAGTGAAT CGTCGTGTTG AAAATGAACT TCAGAAAAAC CGACACAAAC TCAAAAAACA 660
 GGAAAAAGAG TTACTGGCGA CAGACAACGC TGAAGAATTT CGTCAAAAAG GAGAATTGCT 720
 GACAACCTTC CTCCACCAAG TGCCTAACGA CCAAGACCAG GTTATCCTAG ACAACTACTA 780
 TACCAACCAA CCTATCATGA TTGCGCTTGA TAAGGCTCTG ACTCCCAACC AGAATGCCCA 840
 ACGCTATTTT AAACGGTATC AGAAACTCAA AGAAGCTGTC AAATACTTGA CTGATTTGAT 900
 TGAAGAAACC AAAGCCACTA TTCTCTATCT GGAAAGTGTA GAAACCGTCC TCAACCAAGC 960
 TGGACTGGAA GAAATCGCTG AAATCCGTGA AGAATTGATT CAAACAGGTT TTATCCGCAG 1020
 AAGACAACGG GAGAAAAATCC AGAAACGCAA AAAACTAGAA CAATATCTAG CAAGCGATGG 1080
 CAAAACCATC ATCTATGTCG GACGAAACAA TCTTCAAAAT GAGGAATTGA CCTTTAAAAAT 1140
 GGCCCGCAAG GAGGAACTTT GGTTCATGCG TAAGGACATT CCTGGAAGCC ATGTTGTCAT 1200
 CTCAGGAAAT CTTGACCCAT CTGATGCAGT CAAGACAGAC GCAGCAGAGT TAGCTGCCTA 1260
 CTTCTCTCAA GGGCGCCTGT CGAATCTGGT GCAGGTAGAT ATGATTGAAG TCAAAAAACT 1320
 CAATAAACCA ACTGGTGGAA AACCCGGCTT TGTCACCTAC ACAGGACAAA AGACCCTCCG 1380
 CGTCACACCA GACTCCAAAA AAATTGCATC CATGAAAAAA TCC 1423

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Val Leu Arg Lys Tyr Leu Gln Gly Ala Leu Ile Glu Ser Ile Glu Gln
 1 5 10 15

Val Glu Asn Asp Arg Ile Val Glu Ile Thr Val Ser Asn Lys Asn Glu
 20 25 30

Ile Gly Asp His Ile Gln Ala Thr Leu Ile Ile Glu Ile Met Gly Lys
 35 40 45

His Ser Asn Ile Leu Leu Val Asp Lys Ser Ser His Lys Ile Leu Glu
 50 55 60

Val Ile Lys His Val Gly Phe Ser Gln Asn Ser Tyr Arg Thr Leu Leu
 65 70 75 80

Pro Gly Ser Thr Tyr Ile Ala Pro Pro Ser Thr Lys Ser Leu Asn Pro

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Phe Thr Ile Lys Asp Glu Lys Leu Phe Glu Ile Leu Gln Thr Gln Glu
 100 105 110
 Leu Thr Ala Lys Asn Leu Gln Ser Leu Phe Gln Gly Leu Gly Arg Asp
 115 120 125
 Thr Ala Asn Glu Leu Glu Arg Ile Leu Val Ser Glu Lys Leu Ser Ala
 130 135 140
 Phe Arg Asn Phe Phe Asn Gln Glu Thr Lys Pro Cys Leu Thr Glu Thr
 145 150 155 160
 Ser Phe Ser Pro Val Pro Phe Ala Asn Gln Val Gly Glu Pro Phe Ala
 165 170 175
 Asn Leu Ser Asp Leu Leu Asp Thr Tyr Tyr Lys Asp Lys Ala Glu Arg
 180 185 190
 Asp Arg Val Lys Gln Gln Ala Ser Glu Leu Ile Arg Arg Val Glu Asn
 195 200 205
 Glu Leu Gln Lys Asn Arg His Lys Leu Lys Lys Gln Glu Lys Glu Leu
 210 215 220
 Leu Ala Thr Asp Asn Ala Glu Glu Phe Arg Gln Lys Gly Glu Leu Leu
 225 230 235 240
 Thr Thr Phe Leu His Gln Val Pro Asn Asp Gln Asp Gln Val Ile Leu
 245 250 255
 Asp Asn Tyr Tyr Thr Asn Gln Pro Ile Met Ile Ala Leu Asp Lys Ala
 260 265 270
 Leu Thr Pro Asn Gln Asn Ala Gln Arg Tyr Phe Lys Arg Tyr Gln Lys
 275 280 285
 Leu Lys Glu Ala Val Lys Tyr Leu Thr Asp Leu Ile Glu Glu Thr Lys
 290 295 300
 Ala Thr Ile Leu Tyr Leu Glu Ser Val Glu Thr Val Leu Asn Gln Ala
 305 310 315 320
 Gly Leu Glu Glu Ile Ala Glu Ile Arg Glu Glu Leu Ile Gln Thr Gly
 325 330 335
 Phe Ile Arg Arg Arg Gln Arg Glu Lys Ile Gln Lys Arg Lys Lys Leu
 340 345 350
 Glu Gln Tyr Leu Ala Ser Asp Gly Lys Thr Ile Ile Tyr Val Gly Arg
 355 360 365
 Asn Asn Leu Gln Asn Glu Glu Leu Thr Phe Lys Met Ala Arg Lys Glu
 370 375 380
 Glu Leu Trp Phe His Ala Lys Asp Ile Pro Gly Ser His Val Val Ile
 385 390 395 400
 Ser Gly Asn Leu Asp Pro Ser Asp Ala Val Lys Thr Asp Ala Ala Glu
 405 410 415
 Leu Ala Ala Tyr Phe Ser Gln Gly Arg Leu Ser Asn Leu Val Gln Val

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425

430

Asp Met Ile Glu Val Lys Lys Leu Asn Lys Pro Thr Gly Gly Lys Pro
 435 440 445

Gly Phe Val Thr Tyr Thr Gly Gln Lys Thr Leu Arg Val Thr Pro Asp
 450 455 460

Ser Lys Lys Ile Ala Ser Met Lys Lys Ser
 465 470

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACAACATTT ACTATCCATA CAGTAGAGTC AGCACCAGCA GAAGTGAAAG AAATTCTTGA 60
 AACAGTAGAA AAAGACAACA ATGGCTATAT TCCCAACCTA ATCGGTCTCT TGGCCAATGC 120
 CCCGACTGTT TTAGAAGCCT ACCAAATTGT CTCATCTATC CACCGTCGCA ACAGCCTGAC 180
 ACCCGTTGAG CGTGAAGTGG TGCAAATCAC GGCAGCCGTG ACCAATGGTT GTGCCTTCTG 240
 TGTGCGAGGT CACACAGCCT TTTCCATCAA ACAAATCCAG ATGAATGATG ACTTGATTCA 300
 AGCTCTTCGC AATCGTACTC CAATTGAAAC AGATCCTAAA TTGGATACCC TAGCTAAGTT 360
 TACCTTGGCA GTTATCAATA CCAAGGGTCG TGTAGGAGAT GAAGCCTTGT CTGAGTTTTT 420
 AGAAGCTGGC TACACTCAAC AAAATGCCTT GGATGTGGTT TTTGGTGTCA GCCTAGCAAT 480
 CCTCTGTAAC TATGCCAACA ACTTAGCTAA TACACCAATT AATCCAGAAT TGCAACCTTA 540
 TGCC 544

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr Thr Phe Thr Ile His Thr Val Glu Ser Ala Pro Ala Glu Val Lys
 1 5 10 15
 Glu Ile Leu Glu Thr Val Glu Lys Asp Asn Asn Gly Tyr Ile Pro Asn
 20 25 30
 Leu Ile Gly Leu Leu Ala Asn Ala Pro Thr Val Leu Glu Ala Tyr Gln

35	40	45
Ile Val Ser Ser Ile His Arg Arg Asn Ser Leu Thr Pro Val Glu Arg		
50	55	60
Glu Val Val Gln Ile Thr Ala Ala Val Thr Asn Gly Cys Ala Phe Cys		
65	70	75 80
Val Ala Gly His Thr Ala Phe Ser Ile Lys Gln Ile Gln Met Asn Asp		
	85	90 95
Asp Leu Ile Gln Ala Leu Arg Asn Arg Thr Pro Ile Glu Thr Asp Pro		
	100	105 110
Lys Leu Asp Thr Leu Ala Lys Phe Thr Leu Ala Val Ile Asn Thr Lys		
	115	120 125
Gly Arg Val Gly Asp Glu Ala Leu Ser Glu Phe Leu Glu Ala Gly Tyr		
	130	135 140
Thr Gln Gln Asn Ala Leu Asp Val Val Phe Gly Val Ser Leu Ala Ile		
	145	150 155 160
Leu Cys Asn Tyr Ala Asn Asn Leu Ala Asn Thr Pro Ile Asn Pro Glu		
	165	170 175
Leu Gln Pro Tyr Ala		
	180	

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGCTAAGGAA AGAGTGGATG TACTAGCTTA TAAACAGGGG TTGTTTGAAA CGAGAGAGCA	60
GGCCAAGCGA GGTGTGATGG CTGGCCTAGT CGTAGCAGTC CTTAATGGAG AACGGTTTGA	120
CAAGCCAGGA GAGAAAATTC CAGATGACAC CGAATTAAAA CTCAAGGGGG AGAAACTCAA	180
GTATGTCAGC CGTGGTGGTT TGAAACTGGA AAAGGCCTTG CAGGTCTTTG ATTTGTCGGT	240
GGATGGCGCG ACTACGATTG ATATCGGGGC CTCTACTGGA GGTTTTACCG ATGTCATGCT	300
ACAGAATAGT GCCAAGTTGG TCTTTGCAGT CGATGTTGGT ACCAATCAGT TGGCTTGGAA	360
ATTACGCCAA GACCCACGAG TTGTCAGCAT GGAGCAGTTC AATTTCCGCT ATGCTGAAAA	420
GA CTGATTTT CAGCAGGAGC CGAGCTTTGC CAGTATTGAT GTGAGTTTCA TTTCCCTTAG	480
TCTGATTTTG CCAGCCTTGC ACCGTGTCTT GGCTGATCAA GGTCAGGTGG TAGCACTTGT	540
CAAACCTCAG TTTGAGGCAG GACGTGAGCA GATTGGGAAA AATGGAATTA TTCGAGATGC	600
TAAGGTTTCAT CAGAATGTCC TTGAATCTGT AACAGCTATG GCAGTAGAGG TAGGTTTTTC	660

(2) INFORMATION FOR SEQ ID NO:64:

(A) LENGTH: 270 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala	Lys	Glu	Arg	Val	Asp	Val	Leu	Ala	Tyr	Lys	Gln	Gly	Leu	Phe	Glu
1				5					10					15
Thr	Arg	Glu	Gln	Ala	Lys	Arg	Gly	Val	Met	Ala	Gly	Leu	Val	Val	Ala
			20					25					30		
Val	Leu	Asn	Gly	Glu	Arg	Phe	Asp	Lys	Pro	Gly	Glu	Lys	Ile	Pro	Asp
		35					40					45			
Asp	Thr	Glu	Leu	Lys	Leu	Lys	Gly	Glu	Lys	Leu	Lys	Tyr	Val	Ser	Arg
	50					55					60				
Gly	Gly	Leu	Lys	Leu	Glu	Lys	Ala	Leu	Gln	Val	Phe	Asp	Leu	Ser	Val
65					70					75					80
Asp	Gly	Ala	Thr	Thr	Ile	Asp	Ile	Gly	Ala	Ser	Thr	Gly	Gly	Phe	Thr
				85					90					95	
Asp	Val	Met	Leu	Gln	Asn	Ser	Ala	Lys	Leu	Val	Phe	Ala	Val	Asp	Val
			100					105					110		
Gly	Thr	Asn	Gln	Leu	Ala	Trp	Lys	Leu	Arg	Gln	Asp	Pro	Arg	Val	Val
		115					120					125			
Ser	Met	Glu	Gln	Phe	Asn	Phe	Arg	Tyr	Ala	Glu	Lys	Thr	Asp	Phe	Glu
	130					135					140				
Gln	Glu	Pro	Ser	Phe	Ala	Ser	Ile	Asp	Val	Ser	Phe	Ile	Ser	Leu	Ser
145					150					155					160
Leu	Ile	Leu	Pro	Ala	Leu	His	Arg	Val	Leu	Ala	Asp	Gln	Gly	Gln	Val
				165					170					175	
Val	Ala	Leu	Val	Lys	Pro	Gln	Phe	Glu	Ala	Gly	Arg	Glu	Gln	Ile	Gly
			180					185					190		
Lys	Asn	Gly	Ile	Ile	Arg	Asp	Ala	Lys	Val	His	Gln	Asn	Val	Leu	Glu
		195					200					205			
Ser	Val	Thr	Ala	Met	Ala	Val	Glu	Val	Gly	Phe	Ser	Val	Leu	Gly	Leu
						215					220				
Asp	Phe	Ser	Pro	Ile	Gln	Gly	Gly	His	Gly	Asn	Ile	Glu	Phe	Leu	Ala
225					230					235					240

Tyr Leu Lys Lys Glu Lys Ser Ala Ser Asn Gln Ile Leu Ala Glu Ile
 245 250 255

Lys Glu Ala Val Glu Arg Ala His Ser Gln Phe Lys Asn Glu
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTGTTCTAT GAAGTTGGTC GTCACCAAGC TGGTCAGGTT AAGAAAGAGT CTAATCGAGT	60
TTCTTATATA GATGGTGATC AGGCTGGTCA AAAGGCAGAA AACTTGACAC CAGATGAAGT	120
CAGTAAGAGG GAGGGGATCA ACGCCGAACA AATNGTNATC AAGATTACGG ATCAAGGTTA	180
TGTGACCTCT CATGGAGACC ATTATCATTA CTATAATGGC AAGGTTCTTT ATGATGCCAT	240
CATCAGTGAA GAGCTCCTCA TGAAAGATCC GAATTATCAG TTGAAGGATT CAGACATTGT	300
CAATGAAATC AAGGGTGGTT ATGTCATTAA GGTAACCGGT AAATACTATG TNTACCTTAA	360
GGATGCAGCT CATGCGGATA ATATTCGGAC AAAAGAAGAG ATTAAACGTC AGAAGCAGGA	420
ACGCAGTCAT AATCATAACT CAAGAGCAGA TAATGCTGTT GCTGCAGCCA GAGCCCAAGG	480
ACGTTATACA ACGGATGATG GGTATATCTT CAATGCATCT GATATCATTG AGGACACGGG	540
TGATGCTTAT ATCGTTCTC ACGGCGACCA TTACCATTAC ATTCCTAAGA ATGAGTTATC	600
AGCTAGCGAG TTAGCTGCTG CAGAAGCCTA TTGGAATGGG AAGCAGGGAT CTCGTCCTTC	660
TTCAAGTTCT AGTTATAATG CAAATCCAGC TCAACCAAGA TTGTCAGAGA ACCACAATCT	720
GACTGTCACT CCAACTTATC ATCAAAATCA AGGGGAAAAC ATTTCAAGCC TTTTACGTGA	780
ATTGTATGCT AAACCTTAT CAGAACGCCA TGTGGAATCT GATGGCCTTA TTTTCGACCC	840
AGCGCAAATC ACAAGTCGAA CCGCCAGAGG TGTAGCTGTC CCTCATGGTA ACCATTACCA	900
CTTTATCCCT TATGAACAAA TGTCTGAATT GGAAAAACGA ATTGCTCGTA TTATCCCCCT	960
TCGTTATCGT TCAAACCAT TGGTACCAGA TTCAAGACCA GAACAACCAA GTCCACAATC	1020
GACTCCGGAA CCTAGTCCAA GTCCGCAACC TGCACCAAAT CCTCAACCAG CTCCAAGCAA	1080
TCCAATTGAT GAGAAATTGG TCAAAGAAGC TGTTTGAAAA GTAGGCGATG GTTATGTCTT	1140
TGAGGAGAAT GGAGTTTCTC GTTATATCCC AGCCAAGGAT CTTTCAGCAG AAACAGCAGC	1200
AGGCATTGAT AGCAAACCTGG CCAAGCAGGA AAGTTTATCT CATAAGCTAG GAGCTAAGAA	1260
AACTGACCTC CCATCTAGTG ATCGAGAATT TTACAATAAG GCTTATGACT TACTAGCAAG	1320

AATTCACCAA GATTTACTTG ATAATAAAGG TCGACAAGTT GATTTTGAGG CTTTGGATAA 1380
 CCTGTTGGAA CGACTCAAGG ATGTCNCAAG TGATAAAGTC AAGTTAGTGG ANGATATTCT 1440
 TGCCTTCTTA GCTCCGATTC GTCATCCAGA ACGTTTtagga AAACCAAATG CGCAAATTAC 1500
 CTACACTGAT GATGAGATTC AAGTAGCCAA GTTGGCAGGC AAGTACACAA CAGAAGACGG 1560
 TTATATCTTT GATCCTCGTG ATATAACCAG TGATGAGGGG GATGCCTATG TAACTCCACA 1620
 TATGACCCAT AGCCACTGGA TTAAAAAGA TAGTTTGTCT GAAGCTGAGA GAGCGGCAGC 1680
 CCAGGCTTAT GCTAAAGAGA AAGGTTTGAC CCCTCCTTCG ACAGACCATC AGGATTCAGG 1740
 AAATACTGAG GCAAAAGGAG CAGAAGCTAT CTACAACCGC GTGAAAGCAG CTAAGAAGGT 1800
 GCCACTTGAT CGTATGCCTT ACAATCTTCA ATATACTGTA GAAGTCAAAA ACGGTAGTTT 1860
 AATCATACCT CATTATGACC ATTACCATAA CATCAAATTT GAGTGGTTTG ACGAAGGCCT 1920
 TTATGAGGCA CCTAAGGGGT ATACTCTTGA GGATCTTTTG GCGACTGTCA AGTACTATGT 1980
 CGAACATCCA AACGAACGTC CGCATTCAGA TAATGGTTTT GGTAAACGCTA GCGACCATGT 2040
 TCAAAGAAAC AAAAATGGTC AAGCTGATAC CAATCAAACG GAAAAACCAA GCGAGGAGAA 2100
 ACCTCAGACA GAAAAACCTG AGGAAGAAAC CCCTCGAGAA GAGAAACCGC AAAGCGAGAA 2160
 ACCAGAGTCT CCAAACCAA CAGAGGAACC AGAAGAATCA CCAGAGGAAT CAGAAGAACC 2220
 TCAGGTCGAG ACTGAAAAGG TTGAAGAAAA ACTGAGAGAG GCTGAAGATT TACTTGAAAA 2280
 AATCCAGGAT 2290

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Xaa Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp

420

425

430

Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn
 435 440 445

Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg
 450 455 460

Leu Lys Asp Val Xaa Ser Asp Lys Val Lys Leu Val Xaa Asp Ile Leu
 465 470 475 480

Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn
 485 490 495

Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 500 505 510

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile
 515 520 525

Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser
 530 535 540

His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala
 545 550 555 560

Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His
 565 570 575

Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn
 580 585 590

Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn
 595 600 605

Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His
 610 615 620

Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu
 625 630 635 640

Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val
 645 650 655

Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly
 660 665 670

Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala
 675 680 685

Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu
 690 695 700

Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys
 705 710 715 720

Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Ser Pro Glu Glu
 725 730 735

Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg
 740 745 750

Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp

755

760

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

TTATAAGGGT GAATTAGAAA AAGGATACCA ATTTGATGGT TGGGAAATTT CTGGTTTCGA      60
AGGTAAAAAA GACGCTGGCT ATGTTATTAA TCTATCAAAA GATACCTTTA TAAACCTGT      120
ATTCAAGAAA ATAGAGGAGA AAAAGGAGGA AGAAAATAAA CCTACTTTTG ATGTATCGAA      180
AAAGAAAGAT AACCCACAAG TAAACCATAG TCAATTAAAT GAAAGTCACA GAAAAGAGGA      240
TTTACAAAGA GAAGAGCATT CACAAAAATC TGATTCAACT AAGGATGTTA CAGCTACAGT      300
TCTTGATAAA AACAATATCA GTAGTAAATC AACTACTAAC AATCCTAATA AG              352

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(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Tyr Lys Gly Glu Leu Glu Lys Gly Tyr Gln Phe Asp Gly Trp Glu Ile
1          5          10          15
Ser Gly Phe Glu Gly Lys Lys Asp Ala Gly Tyr Val Ile Asn Leu Ser
20        25        30
Lys Asp Thr Phe Ile Lys Pro Val Phe Lys Lys Ile Glu Lys Lys
35        40        45
Glu Glu Glu Asn Lys Pro Thr Phe Asp Val Ser Lys Lys Lys Asp Asn
50        55        60
Pro Gln Val Asn His Ser Gln Leu Asn Glu Ser His Arg Lys Glu Asp
65        70        75        80
Leu Gln Arg Glu Glu His Ser Gln Lys Ser Asp Ser Thr Lys Asp Val
85        90        95
Thr Ala Thr Val Leu Asp Lys Asn Asn Ile Ser Ser Lys Ser Thr Thr
100       105       110
Asn Asn Pro Asn Lys
115

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(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GAATGTTTCAG GCTCAAGAAA GTTCAGGAAA TAAAATCCAC TTTATCAATG TTCAAGAAGG	60
TGGCAGTGAT GCGATTATTC TTGAAAGCAA TGGACATTTT GCCATGGTGG ATACAGGAGA	120
AGATTATGAT TTCCCAGATG GAAGTGATTC TCGCTATCCA TGGAGAGAAG GAATTGAAAC	180
GTCTTATAAG CATGTTCTAA CAGACCGTGT CTTTCGTCGT TTGAAGGAAT TGGGTGTCCA	240
AAAACTTGAT TTTATTTTGG TGACCCATAC CCACAGTGAT CATATTGGAA ATGTTGATGA	300
ATTACTGTCT ACCTATCCAG TTGACCGAGT CTATCTTAAG AAATATAGTG ATAGTCGTAT	360
TACTAATTCT GAACGTCTAT GGGATAATCT GTATGGCTAT GATAAGGTTT TACAGACTGC	420
TGCAGAAAAA GGTGTTTCAG TTATTCAAAA TATCACACAA GGGGATGCTC ATTTTCAGTT	480
TGGGGACATG GATATTCAGC TCTATAATTA TGAAAATGAA ACTGATTCAT CGGGTGAATT	540
AAAGAAAATT TGGGATGACA ATTCCAATTC CTTGATTAGC GTGGTGAAAG TCAATGGCAA	600
GAAAATTTAC CTTGGGGGCG ATTTAGATAA TGTTCATGGA GCAGAAGACA AGTATGGTCC	660
TCTCATTGGA AAAGTTGATT TGATGAAGTT TAATCATCAC CATGATACCA ACAAATCAAA	720
TACCAAGGAT TTCATTAAAA ATTTGAGTCC GAGTTTGATT GTTCAAACTT CGGATAGTCT	780
ACCTTGGAAT AATGGTGTTG ATAGTGAGTA TGTTAATTGG CTCAAAGAAC GAGGAATTGA	840
GAGAATCAAC GCAGCCAGCA AAGACTATGA TGCAACAGTT TTTGATATTC GAAAAGACGG	900
TTTTGTCAAT ATTTCAACAT CCTACAAGCC GATTCCAAGT TTTCAAGCTG GTTGGCATAA	960
GAGTGCATAT GGGAACTGGT GGTATCAAGC GCCTGATTCT ACAGGAGAGT ATGCTGTCTGG	1020
TTGGAATGAA ATCGAAGGTG AATGGTATTA CTTTAACCAA ACGGGTATCT TGTTACAGAA	1080
TCAATGGAAA AAATGGAACA ATCATTGGTT CTATTTGACA GACTCTGGTG CTTCTGCTAA	1140
AAATTGGAAG AAAATCGCTG GAATCTGGTA TTATTTTAAC AAAGAAAACC AGATGGAAAT	1200
TGGTTGGATT CAAGATAAAG AGCAGTGATA TTATTTGGAT GTTGATGGTT CTATGAAGAC	1260
AGGATGGCTT CAATATATGG GGCAATGGTA TTAATTTGCT CCATCAGGGG AA	1312

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Asn Val Gln Ala Gln Glu Ser Ser Gly Asn Lys Ile His Phe Ile Asn
1          5          10          15
Val Gln Glu Gly Gly Ser Asp Ala Ile Ile Leu Glu Ser Asn Gly His
20          25          30
Phe Ala Met Val Asp Thr Gly Glu Asp Tyr Asp Phe Pro Asp Gly Ser
35          40          45
Asp Ser Arg Tyr Pro Trp Arg Glu Gly Ile Glu Thr Ser Tyr Lys His
50          55          60
Val Leu Thr Asp Arg Val Phe Arg Arg Leu Lys Glu Leu Gly Val Gln
65          70          75          80
Lys Leu Asp Phe Ile Leu Val Thr His Thr His Ser Asp His Ile Gly
85          90          95
Asn Val Asp Glu Leu Leu Ser Thr Tyr Pro Val Asp Arg Val Tyr Leu
100         105         110
Lys Lys Tyr Ser Asp Ser Arg Ile Thr Asn Ser Glu Arg Leu Trp Asp
115         120         125
Asn Leu Tyr Gly Tyr Asp Lys Val Leu Gln Thr Ala Ala Glu Lys Gly
130         135         140
Val Ser Val Ile Gln Asn Ile Thr Gln Gly Asp Ala His Phe Gln Phe
145         150         155         160
Gly Asp Met Asp Ile Gln Leu Tyr Asn Tyr Glu Asn Glu Thr Asp Ser
165         170         175
Ser Gly Glu Leu Lys Lys Ile Trp Asp Asp Asn Ser Asn Ser Leu Ile
180         185         190
Ser Val Val Lys Val Asn Gly Lys Lys Ile Tyr Leu Gly Gly Asp Leu
195         200         205
Asp Asn Val His Gly Ala Glu Asp Lys Tyr Gly Pro Leu Ile Gly Lys
210         215         220
Val Asp Leu Met Lys Phe Asn His His His Asp Thr Asn Lys Ser Asn
225         230         235         240
Thr Lys Asp Phe Ile Lys Asn Leu Ser Pro Ser Leu Ile Val Gln Thr
245         250         255
Ser Asp Ser Leu Pro Trp Lys Asn Gly Val Asp Ser Glu Tyr Val Asn
260         265         270
Trp Leu Lys Glu Arg Gly Ile Glu Arg Ile Asn Ala Ala Ser Lys Asp
275         280         285
Tyr Asp Ala Thr Val Phe Asp Ile Arg Lys Asp Gly Phe Val Asn Ile
290         295         300

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Ser Thr Ser Tyr Lys Pro Ile Pro Ser Phe Gln Ala Gly Trp His Lys
 305 310 315 320

Ser Ala Tyr Gly Asn Trp Trp Tyr Gln Ala Pro Asp Ser Thr Gly Glu
 325 330 335

Tyr Ala Val Gly Trp Asn Glu Ile Glu Gly Glu Trp Tyr Tyr Phe Asn
 340 345 350

Gln Thr Gly Ile Leu Leu Gln Asn Gln Trp Lys Lys Trp Asn Asn His
 355 360 365

Trp Phe Tyr Leu Thr Asp Ser Gly Ala Ser Ala Lys Asn Trp Lys Lys
 370 375 380

Ile Ala Gly Ile Trp Tyr Tyr Phe Asn Lys Glu Asn Gln Met Glu Ile
 385 390 395 400

Gly Trp Ile Gln Asp Lys Glu Gln Trp Tyr Tyr Leu Asp Val Asp Gly
 405 410 415

Ser Met Lys Thr Gly Trp Leu Gln Tyr Met Gly Gln Trp Tyr Tyr Phe
 420 425 430

Ala Pro Ser Gly Glu
 435

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTTGGGTGTA ACCCATATCC AGCTCCTTCC AGTCTTGTCT TACTACTTTG TCAATGAATT	60
GAAAAACCAT GAACGCTTGT CTGACTACGC TTCAAGCAAC AGCAACTACA ACTGGGGATA	120
TGACCCTCAA AACTACTTCT CCTTGACTGG TATGTACTCA AGCGATCCTA AGAATCCAGA	180
AAAACGAATC GCAGAATTTA AAAACCTCAT CAACGAAATC CACAAACGTG GTATGGGAGC	240
TATCCTAGAT GTCGTTTATA ACCACACAGC CAAAGTCGAT CTCTTTGAAG ATTTGGAACC	300
AAACTACTAC CACTTTATGG ATGCCGATGG CACACCTCGA ACTAGCTTTG GTGGTGGACG	360
CTTGGGGACA ACCCACCATA TGACCAAACG GCTCCTAATT GACTCTATCA AATACCTAGT	420
TGATACCTAC AAAGTGGATG GCTTCCGTTT CGATATGATG GGAGACCATG ACGCCGCTTC	480
TATCGAAGAA GCTTACAAGG CTGCACGCGC CCTCAATCCA AACCTCATCA TGCTTGGTGA	540
AGGTTGGAGA ACCTATGCCG GTGATGAAAA CATGCCTACT AAAGCTGCTG ACCAAGATTG	600
GATGAAACAT ACCGATACTG TCGCTGTCTT TTCAGATGAC ATCCGTAACA ACCTCAAATC	660
TGGTTATCCA AACGAAGGTC AACCTGCCTT TATCACAGGT GGCAAGCGTG ATGTCAACAC	720

CATCTTTAAA AATCTCATTG CTCAACCAAC TAACTTTGAA GCTGACAGCC CTGGAGATGT 780
 CATCCAATAC ATCGCAGCCC ATGATAACTT GACCCCTCTTT GACATCATTG CCCAGTCTAT 840
 CAAAAAAGAC CCAAGCAAGG CTGAGAACTA TGCTGAAATC CACCGTCGTT TACGACTTGG 900
 AAATCTCATG GTCTTGACAG CTCAAGGAAC TCCATTATATC CACTCCGGTC AGGAATATGG 960
 ACGTACTAAA CAATTCCGTG ACCCAGCCTA CAAGACTCCA GTAGCAGAGG ATAAGGTTCC 1020
 AAACAAATCT CACTTGTTGC GTGATAAGGA CGGCAACCCA TTTGACTATC CTTACTTCAT 1080
 CCATGACTCT TACGATTCTA GTGATGCAGT CAACAAGTTT GACTGGACTA AGGCTACAGA 1140
 TGGTAAAGCT TATCCTGAAA ATGTCAAGAG CCGTGACTAT ATGAAAGGTT TGATTGCCCT 1200
 TCGTCAATCT ACAGATGCCT TCCGACTTAA GAGTCTTCAA GATATCAAAG ACCGTGTCCA 1260
 CCTCATCACT GTCCCAGGCC AAAATGGTGT GGAAAAAGAG GATGTAGTGA TTGGCTACCA 1320
 AATCACTGCT CCAAACGGCG ATATCTACGC AGTCTTTGTC AATGCGGATG AAAAAGCTCG 1380
 CGAATTTAAT TTGGGAACTG CCTTTGCACA TCTAAGAAAT GCGGAAGTTT TGGCAGATGA 1440
 AAACCAAGCA GGACCAGTCG GAATTGCCAA CCCGAAAGGA CTTGAATGGA CTGAAAAAGG 1500
 CTTGAAATTG AATGCCCTTA CAGCTACTGT TCTTCGAGTC TCTCAAATG GAACTAGCCA 1560
 TGAGTCAACT GCAGAAGAGA AACCAGACTC AACCCTTCC AAGCCTGAAC ATCAAATGA 1620
 AGCTTCTCAC CCTGCACATC AAGACCCAGC TCCAGAAGCT AGACCTGATT CTACTAAACC 1680
 AGATGCCAAA GTAGCTGATG CGGAAAATAA ACCTAGCCAA GCTACAGCTG ATTCACAAGC 1740
 TGAACAACCA GCACAAGAAG CACAAGCATC ATCTGTAAAA GAAGCGGTTC GAAACGAATC 1800
 GGTAGAAAAC TCTAGCAAGG AAAATATACC TGCAACCCCA GATAACAAG CTGAA 1855

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 618 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu	Gly	Val	Thr	His	Ile	Gln	Leu	Leu	Pro	Val	Leu	Ser	Tyr	Tyr	Phe
1				5					10					15	
Val	Asn	Glu	Leu	Lys	Asn	His	Glu	Arg	Leu	Ser	Asp	Tyr	Ala	Ser	Ser
		20						25					30		
Asn	Ser	Asn	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Gln	Asn	Tyr	Phe	Ser	Leu
		35					40					45			
Thr	Gly	Met	Tyr	Ser	Ser	Asp	Pro	Lys	Asn	Pro	Glu	Lys	Arg	Ile	Ala
		50				55					60				

Glu	Phe	Lys	Asn	Leu	Ile	Asn	Glu	Ile	His	Lys	Arg	Gly	Met	Gly	Ala
65					70					75					80
Ile	Leu	Asp	Val	Val	Tyr	Asn	His	Thr	Ala	Lys	Val	Asp	Leu	Phe	Glu
			85						90					95	
Asp	Leu	Glu	Pro	Asn	Tyr	Tyr	His	Phe	Met	Asp	Ala	Asp	Gly	Thr	Pro
			100					105					110		
Arg	Thr	Ser	Phe	Gly	Gly	Gly	Arg	Leu	Gly	Thr	Thr	His	His	Met	Thr
		115					120					125			
Lys	Arg	Leu	Leu	Ile	Asp	Ser	Ile	Lys	Tyr	Leu	Val	Asp	Thr	Tyr	Lys
	130					135					140				
Val	Asp	Gly	Phe	Arg	Phe	Asp	Met	Met	Gly	Asp	His	Asp	Ala	Ala	Ser
145					150					155					160
Ile	Glu	Glu	Ala	Tyr	Lys	Ala	Ala	Arg	Ala	Leu	Asn	Pro	Asn	Leu	Ile
				165					170					175	
Met	Leu	Gly	Glu	Gly	Trp	Arg	Thr	Tyr	Ala	Gly	Asp	Glu	Asn	Met	Pro
			180					185					190		
Thr	Lys	Ala	Ala	Asp	Gln	Asp	Trp	Met	Lys	His	Thr	Asp	Thr	Val	Ala
		195					200					205			
Val	Phe	Ser	Asp	Asp	Ile	Arg	Asn	Asn	Leu	Lys	Ser	Gly	Tyr	Pro	Asn
	210					215					220				
Glu	Gly	Gln	Pro	Ala	Phe	Ile	Thr	Gly	Gly	Lys	Arg	Asp	Val	Asn	Thr
225					230					235					240
Ile	Phe	Lys	Asn	Leu	Ile	Ala	Gln	Pro	Thr	Asn	Phe	Glu	Ala	Asp	Ser
			245						250					255	
Pro	Gly	Asp	Val	Ile	Gln	Tyr	Ile	Ala	Ala	His	Asp	Asn	Leu	Thr	Leu
			260					265					270		
Phe	Asp	Ile	Ile	Ala	Gln	Ser	Ile	Lys	Lys	Asp	Pro	Ser	Lys	Ala	Glu
		275					280					285			
Asn	Tyr	Ala	Glu	Ile	His	Arg	Arg	Leu	Arg	Leu	Gly	Asn	Leu	Met	Val
	290					295					300				
Leu	Thr	Ala	Gln	Gly	Thr	Pro	Phe	Ile	His	Ser	Gly	Gln	Glu	Tyr	Gly
305					310					315					320
Arg	Thr	Lys	Gln	Phe	Arg	Asp	Pro	Ala	Tyr	Lys	Thr	Pro	Val	Ala	Glu
			325						330					335	
Asp	Lys	Val	Pro	Asn	Lys	Ser	His	Leu	Leu	Arg	Asp	Lys	Asp	Gly	Asn
			340					345					350		
Pro	Phe	Asp	Tyr	Pro	Tyr	Phe	Ile	His	Asp	Ser	Tyr	Asp	Ser	Ser	Asp
		355					360					365			
Ala	Val	Asn	Lys	Phe	Asp	Trp	Thr	Lys	Ala	Thr	Asp	Gly	Lys	Ala	Tyr
		370				375					380				
Pro	Glu	Asn	Val	Lys	Ser	Arg	Asp	Tyr	Met	Lys	Gly	Leu	Ile	Ala	Leu
385					390					395					400

Arg Gln Ser Thr Asp Ala Phe Arg Leu Lys Ser Leu Gln Asp Ile Lys
 405 410 415
 Asp Arg Val His Leu Ile Thr Val Pro Gly Gln Asn Gly Val Glu Lys
 420 425 430
 Glu Asp Val Val Ile Gly Tyr Gln Ile Thr Ala Pro Asn Gly Asp Ile
 435 440 445
 Tyr Ala Val Phe Val Asn Ala Asp Glu Lys Ala Arg Glu Phe Asn Leu
 450 455 460
 Gly Thr Ala Phe Ala His Leu Arg Asn Ala Glu Val Leu Ala Asp Glu
 465 470 475 480
 Asn Gln Ala Gly Pro Val Gly Ile Ala Asn Pro Lys Gly Leu Glu Trp
 485 490 495
 Thr Glu Lys Gly Leu Lys Leu Asn Ala Leu Thr Ala Thr Val Leu Arg
 500 505 510
 Val Ser Gln Asn Gly Thr Ser His Glu Ser Thr Ala Glu Glu Lys Pro
 515 520 525
 Asp Ser Thr Pro Ser Lys Pro Glu His Gln Asn Glu Ala Ser His Pro
 530 535 540
 Ala His Gln Asp Pro Ala Pro Glu Ala Arg Pro Asp Ser Thr Lys Pro
 545 550 555 560
 Asp Ala Lys Val Ala Asp Ala Glu Asn Lys Pro Ser Gln Ala Thr Ala
 565 570 575
 Asp Ser Gln Ala Glu Gln Pro Ala Gln Glu Ala Gln Ala Ser Ser Val
 580 585 590
 Lys Glu Ala Val Arg Asn Glu Ser Val Glu Asn Ser Ser Lys Glu Asn
 595 600 605
 Ile Pro Ala Thr Pro Asp Lys Gln Ala Glu
 610 615

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TAGTGATGGT ACTTGGCAAG GAAAACAGTA TCTGAAAGAA GATGGCAGTC AAGCAGCAAA	60
TGAGTGGGTT TTNGATACTC ATTATCAATC TTGGTTCTAT ATAAAAGCAG ATGCTAACTA	120
TGCTGAAAAT GAATGGCTAA AGCAAGGTGA CGACTATTTT TACCTCAAAT CTGGTGGCTA	180
TATGGCCAAA TCAGAATGGG TAGAAGACAA GGGAGCCTTT TATTATCTTG ACCAAGATGG	240
AAAGATGAAA AGAAATGCTT GGGTAGGAAC TTCCTATGTT GGTGCAACAG GTGCCAAAGT	300

AATAGAAGAC TGGGTCTATG ATTCTCAATA CGATGCTTGG TTTTATATCA AAGCAGATGG 360
 ACAGCACGCA GAGAAAGAAT GGCTCCAAAT TAAAGGGAAG GACTATTATT TCAAATCCGG 420
 TGGTTATCTA CTGACAAGTC AGTGGATTAA TCAAGCTTAT GTGAATGCTA GTGGTGCCAA 480
 AGTACAGCAA GGTTGGCTTT TTGACAAACA ATACCAATCT TGGTTTTACA TCAAAGAAAA 540
 TGGAACTAT GCTGATAAAG AATGGATTTT CGAGAATGGT CACTATTATT ATCTAAAATC 600
 CGGTGGCTAC ATGGCAGCCA ATGAATGGAT TTGGGATAAG GAATCTTGGT TTTATCTCAA 660
 ATTTGATGGG AAAATGGCTG AAAAAGAATG GGTCTACGAT TCTCATAGTC AAGCTTGGTA 720
 CTACTTCAAA TCCGGTGGTT ACATGACAGC CAATGAATGG ATTTGGGATA AGGAATCTTG 780
 GTTTTACCTC AAATCTGATG GGAAAATAGC TGAAAAAGAA TGGGTCTACG ATTCTCATAG 840
 TCAAGCTTGG TACTACTTCA AATCTGGTGG CTACATGGCG AAAAATGAGA CAGTAGATGG 900
 TTATCAGCTT GGAAGCGATG GTAAATGGCT TGGAGGAAAA ACTACAAATG AAAATGCTGC 960
 TTACTATCAA GTAGTGCCTG TTACAGCCAA TGTTTATGAT TCAGATGGTG AAAAGCTTTC 1020
 CTATATATCG CAAGGTAGTG TCGTATGGCT AGATAAGGAT AGAAAAAGTG ATGACAAGCG 1080
 CTTGGCTATT ACTATTTCTG GTTTGTCAGG CTATATGAAA ACAGAAGATT TACAAGCGCT 1140
 AGATGCTAGT AAGGACTTTA TCCCTTATTA TGAGAGTGAT GGCCACCGTT TTTATCACTA 1200
 TGTGGCTCAG AATGCTAGTA TCCCAGTAGC TTCTCATCTT TCTGATATGG AAGTAGGCAA 1260
 GAAATATTAT TCGGCAGATG GCCTGCATTT TGATGGTTTT AAGCTTGAGA ATCCCTTCCT 1320
 TTTCAAAGAT TTAACAGAGG CTACAACTA CAGTGCTGAA GAATTGGATA AGGTATTTAG 1380
 TTTGCTAAAC ATTAACAATA GCCTTTTGA GAACAAGGGC GCTACTTTTA AGGAAGCCGA 1440
 AGAACATTAC CATATCAATG CTCTTTATCT CCTTGCCCAT AGTGCCCTAG AAAGTAACTG 1500
 GGAAGAAGT AAAATTGCCA AAGATAAGAA TAATTTCTTT GGCATTACAG CCTATGATAC 1560
 GACCCCTTAC CTTTCTGCTA AGACATTTGA TGATGTGGAT AAGGGAATTT TAGGTGCAAC 1620
 CAAGTGGATT AAGGAAAATT ATATCGATAG GGAAGAAGT TTCCTTGGA ACAAGGCTTC 1680
 TGGTATGAAT GTGGAATATG CTTGAGACCC TTATTGGGGC GAAAAAATTG CTAGTGTGAT 1740
 GATGAAAATC AATGAGAAGC TAGGTGGCAA AGAT 1774

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 591 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Asp Gly Thr Trp Gln Gly Lys Gln Tyr Leu Lys Glu Asp Gly Ser
 1 5 10 15
 Gln Ala Ala Asn Glu Trp Val Xaa Asp Thr His Tyr Gln Ser Trp Phe
 20 25 30
 Tyr Ile Lys Ala Asp Ala Asn Tyr Ala Glu Asn Glu Trp Leu Lys Gln
 35 40 45
 Gly Asp Asp Tyr Phe Tyr Leu Lys Ser Gly Gly Tyr Met Ala Lys Ser
 50 55 60
 Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp Gln Asp Gly
 65 70 75 80
 Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val Gly Ala Thr
 85 90 95
 Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln Tyr Asp Ala
 100 105 110
 Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys Glu Trp Leu
 115 120 125
 Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly Tyr Leu Leu
 130 135 140
 Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser Gly Ala Lys
 145 150 155 160
 Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser Trp Phe Tyr
 165 170 175
 Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile Phe Glu Asn
 180 185 190
 Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala Ala Asn Glu
 195 200 205
 Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe Asp Gly Lys
 210 215 220
 Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr
 225 230 235 240
 Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp
 245 250 255
 Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys
 260 265 270
 Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser
 275 280 285
 Gly Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly
 290 295 300
 Ser Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala
 305 310 315 320
 Tyr Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly
 325 330 335

Glu Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys
 340 345 350
 Asp Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu
 355 360 365
 Ser Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys
 370 375 380
 Asp Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr
 385 390 395 400
 Val Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met
 405 410 415
 Glu Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly
 420 425 430
 Phe Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr
 435 440 445
 Asn Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile
 450 455 460
 Asn Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu
 465 470 475 480
 Glu His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu
 485 490 495
 Glu Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe
 500 505 510
 Phe Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr
 515 520 525
 Phe Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys
 530 535 540
 Glu Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser
 545 550 555 560
 Gly Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile
 565 570 575
 Ala Ser Val Met Met Lys Ile Asn Glu Lys Leu Gly Gly Lys Asp
 580 585 590

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:--SEQ ID NO: 75:

TGGGATTCAA TATGTCAGAG ATGATACTAG AGATAAAGAA GAGGGAATAG AGTATGATGA

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CGCTGACAAT GGGGATATTA TTGTAAAAGT AGCGACTAAA CCTAAGGTAG TAACCAAGAA      120
AATTTCAAGT ACGCGAATTC GTTATGAAAA AGATGAAACA AAAGACCGTA GTGAAAATCC      180
TGTTACAATT GATGGAGAGG ATGGCTATGT AACTACGACA AGGACCTACG ATGTTAATCC      240
AGAGACTGGT TATGTTACCG AACAGGTTAC TGTGATAGA AAAGAAGCCA CGGATACAGT      300
TATCAAAGTT CCAGCTAAAA GCAAGGTTGA AGAAGTTCTT GTTCCATTTG CTAATAAATA      360
TGAAGCAGAC AATGACCTTT CTGCAGGACA GGAGCAAGAG ATTACTCTAG GAAAGAATGG      420
GAAAACAGTT ACAACGATAA CTTATAATGT AGATGGAAAG AGTGGACAAG TAACTGAGAG      480
TACTTTAAGT CAAAAAAAAG ACTCtCAAAC AAGAGTTGTT AAAAAAGaA CCArkCCCCA      540
AGTTCTTGTC CAAGAAATTC CAATCGAAAC AGAATATCTC GATGGCCCaA CTCTTGATAA      600
AaGTCAAGAA GTAGAAGAAG TAGGAGAAAT TGGTAAATTA CTCTTACTAC AATCTATACT      660
GGTAGATGAA CGTGATGGAA CAATTGAAGA AACTACTTCT CGTCAAATTA CTAAAGAGAT      720
GGTAAAAAGA CGTATAAGGA GAGGGACGAG AGAACCTGAA AAAGTTGTTG TTCCTGAGCA      780
ATCATCTATT CCTTCGTATC CTGTATCTGT TACATCTAAC CAAGGAACAG ATGTAGCAGT      840
AGAACCAGCT AAAGCAGTTG CTCCAACAAC AGACTGGAAA CAAGAAAATG GTATGTGGTA      900
TTTTTATAAT ACTGATGGTT CCATGGCAAC AGGTTGGGTA CAAGTTAATA GTTCATGGTA      960
CTACCTCAAC AGCAACGGTT CTATGAAAGT CAATCAATGG TTCCAAGTTG GTGGTAAATG     1020
GTATTATGTA AATACATCGG GTGAGTTAGC GGTCAATACA AGTATAGATG GCTATAGAGT     1080
CAATGATAAT GGTGAATGGG TGCCT                                     1105

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(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Gly Ile Gln Tyr Val Arg Asp Asp Thr Arg Asp Lys Glu Glu Gly Ile
1           5           10           15
Glu Tyr Asp Asp Ala Asp Asn Gly Asp Ile Ile Val Lys Val Ala Thr
20           25           30
Lys Pro Lys Val Val Thr Lys Lys Ile Ser Ser Thr Arg Ile Arg Tyr
35           40           45
Glu Lys Asp Glu Thr Lys Asp Arg Ser Glu Asn Pro Val Thr Ile Asp
50           55           60
Gly Glu Asp Gly Tyr Val Thr Thr Thr Arg Thr Tyr Asp Val Asn Pro
65           70           75           80

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Glu Thr Gly Tyr Val Thr Glu Gln Val Thr Val Asp Arg Lys Glu Ala
 85 90 95
 Thr Asp Thr Val Ile Lys Val Pro Ala Lys Ser Lys Val Glu Glu Val
 100 105 110
 Leu Val Pro Phe Ala Thr Lys Tyr Glu Ala Asp Asn Asp Leu Ser Ala
 115 120 125
 Gly Gln Glu Gln Glu Ile Thr Leu Gly Lys Asn Gly Lys Thr Val Thr
 130 135 140
 Thr Ile Thr Tyr Asn Val Asp Gly Lys Ser Gly Gln Val Thr Glu Ser
 145 150 155 160
 Thr Leu Ser Gln Lys Lys Asp Ser Gln Thr Arg Val Val Lys Lys Arg
 165 170 175
 Thr Xaa Pro Gln Val Leu Val Gln Glu Ile Pro Ile Glu Thr Glu Tyr
 180 185 190
 Leu Asp Gly Pro Thr Leu Asp Lys Ser Gln Glu Val Glu Glu Val Gly
 195 200 205
 Glu Ile Gly Lys Leu Leu Leu Leu Gln Ser Ile Leu Val Asp Glu Arg
 210 215 220
 Asp Gly Thr Ile Glu Glu Thr Thr Ser Arg Gln Ile Thr Lys Glu Met
 225 230 235 240
 Val Lys Arg Arg Ile Arg Arg Gly Thr Arg Glu Pro Glu Lys Val Val
 245 250 255
 Val Pro Glu Gln Ser Ser Ile Pro Ser Tyr Pro Val Ser Val Thr Ser
 260 265 270
 Asn Gln Gly Thr Asp Val Ala Val Glu Pro Ala Lys Ala Val Ala Pro
 275 280 285
 Thr Thr Asp Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr
 290 295 300
 Asp Gly Ser Met Ala Thr Gly Trp Val Gln Val Asn Ser Ser Trp Tyr
 305 310 315 320
 Tyr Leu Asn Ser Asn Gly Ser Met Lys Val Asn Gln Trp Phe Gln Val
 325 330 335
 Gly Gly Lys Trp Tyr Tyr Val Asn Thr Ser Gly Glu Leu Ala Val Asn
 340 345 350
 Thr Ser Ile Asp Gly Tyr Arg Val Asn Asp Asn Gly Glu Trp Val Arg
 355 360 365

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGATAATAGA GAAGCATTAA AAACCTTTAT GACGGGTGAA AATTTTATC TCCAACATTA 60
TCTAGGAGCA CATAGGGAAG AACTAAATGG AGAGCATGGC TATACCTTCC GTGTTTGGGC 120
ACCTAATGCT CAGGCTGTTC ACTTGGTTGG TGATTTTACC AACTGGATTG AAAATCAGAT 180
TCCAATGGTA AGAAATGATT TTGGGGTCTG GGAAGTCTTT ACCAATATGG CTCAAGAAGG 240
GCATATTTAC AAATATCATG TCACACGTCA AAATGGTCAT CAACTGATGA AGATTGACCC 300
TTTTGCTGTC AGGTATGAGG CTCGTCCAGG AACAGGGGCA ATCGTAACAG AGCTTCCTGA 360
GAAGAAATGG AAGGATGGAC TTTGGCTGGC ACGAAGAAAA CGTTGGGGCT TTGAAGAGCG 420
TCCTGTCAAT ATTTATGAAG TTCACGCTGG ATCATGGAAA AGAAATTCTG ATGGCAGTCC 480
TTATAGTTTT GCCCAGCTCA AGGATGAACT CATTCTTTAT CTCGTTGAAA TGAACTATAC 540
TCATATTGAG TTTATGCCCT TGATGTCCCA TCCTTTGGGC TTGAGTTGGG GGTATCAGCT 600
TATGGGTTAC TTCGCTTTAG AGCATGCTTA TGGCCGACCA GAGGAGTTTC AAGATTTTGT 660
C 661

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asp Asn Arg Glu Ala Leu Lys Thr Phe Met Thr Gly Glu Asn Phe Tyr
1 5 10 15
Leu Gln His Tyr Leu Gly Ala His Arg Glu Glu Leu Asn Gly Glu His
20 25 30
Gly Tyr Thr Phe Arg Val Trp Ala Pro Asn Ala Gln Ala Val His Leu
35 40 45
Val Gly Asp Phe Thr Asn Trp Ile Glu Asn Gln Ile Pro Met Val Arg
50 55 60
Asn Asp Phe Gly Val Trp Glu Val Phe Thr Asn Met Ala Gln Glu Gly
65 70 75 80
His Ile Tyr Lys Tyr His Val Thr Arg Gln Asn Gly His Gln Leu Met
85 90 95
Lys Ile Asp Pro Phe Ala Val Arg Tyr Glu Ala Arg Pro Gly Thr Gly
100 105 110
Ala Ile Val Thr Glu Leu Pro Glu Lys Lys Trp Lys Asp Gly Leu Trp

115	120	125
Leu Ala Arg Arg Lys Arg Trp Gly Phe Glu Glu Arg Pro Val Asn Ile		
130	135	140
Tyr Glu Val His Ala Gly Ser Trp Lys Arg Asn Ser Asp Gly Ser Pro		
145	150	155 160
Tyr Ser Phe Ala Gln Leu Lys Asp Glu Leu Ile Pro Tyr Leu Val Glu		
	165	170 175
Met Asn Tyr Thr His Ile Glu Phe Met Pro Leu Met Ser His Pro Leu		
	180	185 190
Gly Leu Ser Trp Gly Tyr Gln Leu Met Gly Tyr Phe Ala Leu Glu His		
	195	200 205
Ala Tyr Gly Arg Pro Glu Glu Phe Gln Asp Phe Val		
	210	215 220

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AGATTTTGTC GAGGAGTGTC ATACCCATAA TATTGGGGTT ATTGTGGACT GGGTACCAGN	60
TCACTTTACC ATCAACGATG ATGCCTTAGC CTATTATGAT GGGACACCGA CTTTGAATA	120
CCAAGACCAT AATAAGGCTC ATAACCATGG TTGGGGTGCC CTTAATTTTG ACCTTGAAA	180
AAATGAAGTC CAGTCCTTCT TAATTTCTTG CATTAAGCAT TGGATTGATG TCTATCATTT	240
GGATGGTATT CGTGTGGATG CTGTTAGCAA CATGCTCTAT TTGGACTATG ATGATGCTCC	300
ATGGACACCT AATAAAGATG GCGGAAATCT CAACTATGAA GGTATTATT TCCTTCAGCG	360
CTTGAATGAG GTTATTAAGT TAGAATATCC AGATGTGATG ATGATTGCAG AAGAAAGTTC	420
GTCTGCGATC AAGATTACGG GAATGAAAGA GATTGGTGGT CTAGGATTTG ACTACAAATG	480
GAACATGGGC TGGATGAATG ATATCCTCCG TTTCTACGAA GAAGATCCGA TCTATCGTAA	540
ATATGACTTT AACCTGGTGA CTTTCAGCTT TATGTATGTT TNCAAGGAGA ATTATCTCTT	600
GCCATTCTCG CACGATGAAG TGGTTCATGG CAAGAAGAGT ATGATGCATA AGATGTGGGG	660
AGATCGTTAC AATCAATTCG CAGGCTTGCG CAATCTCTAT ACGTACCAA TTTGTCACCC	720
TGGTAAGAAA TTGCTCTTCA TGGGTAGCGA ATACGGTCAA TTCCTAGAAT GGAAATCTGA	780
AGAACAGTTG GAATGGTCTA ACCTAGAAGA CCCAATGAAT GCTAAGATGA AGTATTTTCG	840
TTCTCAGCTA AACCAGTTTT ACAAAGATCA TCGCTGTCTG TGGGAAATTG ATACCAGCTA	900
TGATGGTATT GAAATCATTG ATGCGGATAA TCGAGACCAG AGTGTTCTTT CCTTTATTCG	960

TAAGGGTAAA AAGGGA

976

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

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Asp Phe Val Glu Glu Cys His Thr His Asn Ile Gly Val Ile Val Asp
1           5           10           15

Trp Val Pro Xaa His Phe Thr Ile Asn Asp Asp Ala Leu Ala Tyr Tyr
          20           25           30

Asp Gly Thr Pro Thr Phe Glu Tyr Gln Asp His Asn Lys Ala His Asn
          35           40           45

His Gly Trp Gly Ala Leu Asn Phe Asp Leu Gly Lys Asn Glu Val Gln
          50           55           60

Ser Phe Leu Ile Ser Cys Ile Lys His Trp Ile Asp Val Tyr His Leu
65           70           75           80

Asp Gly Ile Arg Val Asp Ala Val Ser Asn Met Leu Tyr Leu Asp Tyr
          85           90           95

Asp Asp Ala Pro Trp Thr Pro Asn Lys Asp Gly Gly Asn Leu Asn Tyr
          100          105          110

Glu Gly Tyr Tyr Phe Leu Gln Arg Leu Asn Glu Val Ile Lys Leu Glu
          115          120          125

Tyr Pro Asp Val Met Met Ile Ala Glu Glu Ser Ser Ser Ala Ile Lys
130          135          140

Ile Thr Gly Met Lys Glu Ile Gly Gly Leu Gly Phe Asp Tyr Lys Trp
145          150          155          160

Asn Met Gly Trp Met Asn Asp Ile Leu Arg Phe Tyr Glu Glu Asp Pro
          165          170          175

Ile Tyr Arg Lys Tyr Asp Phe Asn Leu Val Thr Phe Ser Phe Met Tyr
          180          185          190

Val Xaa Lys Glu Asn Tyr Leu Leu Pro Phe Ser His Asp Glu Val Val
          195          200          205

His Gly Lys Lys Ser Met Met His Lys Met Trp Gly Asp Arg Tyr Asn
210          215          220

Gln Phe Ala Gly Leu Arg Asn Leu Tyr Thr Tyr Gln Ile Cys His Pro
225          230          235          240

Gly Lys Lys Leu Leu Phe Met Gly Ser Glu Tyr Gly Gln Phe Leu Glu
          245          250          255

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Trp Lys Ser Glu Glu Gln Leu Glu Trp Ser Asn Leu Glu Asp Pro Met
 260 265 270
 Asn Ala Lys Met Lys Tyr Phe Ala Ser Gln Leu Asn Gln Phe Tyr Lys
 275 280 285
 Asp His Arg Cys Leu Trp Glu Ile Asp Thr Ser Tyr Asp Gly Ile Glu
 290 295 300
 Ile Ile Asp Ala Asp Asn Arg Asp Gln Ser Val Leu Ser Phe Ile Arg
 305 310 315 320
 Lys Gly Lys Lys Gly
 325

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ATCTGTAGTT TATGCGGATG AAACACTTAT TACTCATACT GCTGAGAAAC CTAAAGAGGA 60
 AAAAATGATA GTAGAAGAAA AGGCTGATAA AGCTTTGGAA ACTAAAAATA TAGTTGAAAG 120
 GACAGAACAA AGTGAACCTA GTTCAACTGA GGCTATTGCA TCTGAGNAGA AAGAAGATGA 180
 AGCCGTAACT CCAAAAGAGG AAAAAGTGTC TGCTAAACCG GAAGAAAAAG CTCCAAGGAT 240
 AGAATCACAA GCTTCAAATC AAGAAAAACC GCTCAAGGAA GATGCTAAAG CTGTAACAAA 300
 TGAAGAAGTG AATCAAATGA TTGAAGACAG GAAAGTGGAT TTTAATCAAA ATTGGTACTT 360
 TAAACTCAAT GCAAATTCTA AGGAAGCCAT TAAACCTGAT GCAGACGTAT CTACGTGGAA 420
 AAAATTAGAT TTACCGTATG ACTGGAGTAT CTTTAACGAT TTCGATCATG AATCTCCTGC 480
 ACAAATGAA GGTGGACAGC TCAACGGTGG GGAAGCTTGG TATCGCAAGA CTTTCAAAC 540
 AGATGAAAAA GACCTCAAGA AAAATGTTTCG CCTTACTTTT GATGGCGTCT ACATGGATTC 600
 TCAAGTTTAT GTCAATGGTC AGTTAGTGGG GCATTATCCA AATGGTTATA ACCAGTTCTC 660
 ATATGATATC ACCAAATACC TTCAAAAAGA TGGTCGTGAG AATGTGATTG CTGTCCATGC 720
 AGTCAACAAA CAGCCAAGTA GCCGTTGGTA TTCAGGAAGT GGTATCTATC GTGATGTGAC 780
 TTTACAAGTG ACAGATAAGG TGCATGTTGA GAAAAATGGG ACAACTATTT TAACACCAAA 840
 ACTTGAAGAA CAACAACATG GCAAGGTTGA AACTCATGTG ACCAGCAAAA TCGTCAATAC 900
 GGACGACAAA GACCATGAAC TTGTAGCCGA ATATCAAATC GTTGAACGAG GTGGTCATGC 960
 TGTAACAGGC TTAGTTCGTA CAGCGAGTCG TACCTTAAAA GCACATGAAT CAACAAGCCT 1020
 AGATGCGATT TTAGAAGTTG AAAGACCAAA ACTCTGGACT GTTTTAAATG ACAAACCTGC 1080

CTTGTACGAA TTGATTACGC GTGTTTACCG TGACGGTCAA TTGGTTGATG CTAAGAAGGA 1140
 TTTGTTTGGT TACCGTTACT ATCACTGGAC TCCAAATGAA GGTTCCTCTT TGAATGGTGA 1200
 ACGTATTAAA TTCCATGGAG TATCCTTGCA CCACGACCAT GGGGCGCTTG GAGCAGAAGA 1260
 AACTATAAA GCAGAATATC GCCGTCTCAA ACAAATGAAG GAGATGGGAG TTAAGTCCAT 1320
 CCGTACAACC CACAACCCTG CTAGTGAGCA AACCTTGCAA ATCGCAGCAG AACTAGGTTT 1380
 ACTCGTTCAG GAAGAGGCCT TTGATACGTG GTATGGTGGC AAGAAACCTT ATGACTATGG 1440
 ACGTTTCTTT GAAAAAGATG CCACTCACCC AGAAGCTCGA AAAGGTGAAA AATGGTCTGA 1500
 TTTTGACCTA CGTACCATGG TCGAAAGAGG CAAAAACAAC CCTGCTATCT TCATGTGGTC 1560
 AATTGGTAAT GAAATAGGTG AAGCTAATGG TGATGCCAC TCTTTAGCAA CTGTTAAACG 1620
 TTTGGTTAAG GTTATCAAGG ATGTTGATAA GACTCGCTAT GTTACCATGG GAGCAGATAA 1680
 ATTCCGTTTC GGTAATGGTA GCGGAGGGCA TGAGAAAATT GCTGATGAAC TCGATGCTGT 1740
 TGGATTTAAC TATTCTGAAG ATAATTACAA AGCCCTTAGA GCTAAGCATC CAAAATGGTT 1800
 GATTTATGGA TCAGAAACAT CTTAGCTAC CCGTACACGT GGAAGTTACT ATCGCCCTGA 1860
 ACGTGAATTG AAACATAGCA ATGGACCTGA GCGTAATTAT GAACAGTCAG ATTATGGAAA 1920
 TGATCGTGTG GGTGGGGGA AAACAGCAAC CGCTTCATGG ACTTTTGACC GTGACAACGC 1980
 TGGCTATGCT GGACAGTTTA TCTGGACAGG TACGGACTAT ATTGGTGAAC CTACACCATG 2040
 GCACAACCAA AATCAAATC CTGTTAAGAG CTCTTACTTT GGTATCGTAG ATACAGCCGG 2100
 CATTCCAAA CATGACTTCT ATCTCTACCA AAGC 2134

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Val Val Tyr Ala Asp Glu Thr Leu Ile Thr His Thr Ala Glu Lys
 1 5 10 15
 Pro Lys Glu Glu Lys Met Ile Val Glu Glu Lys Ala Asp Lys Ala Leu
 20 25 30
 Glu Thr Lys Asn Ile Val Glu Arg Thr Glu Gln Ser Glu Pro Ser Ser
 35 40 45
 Thr Glu Ala Ile Ala Ser Glu Xaa Lys Glu Asp Glu Ala Val Thr Pro
 50 55 60
 Lys Glu Glu Lys Val Ser Ala Lys Pro Glu Glu Lys Ala Pro Arg Ile

65		70		75		80
Glu Ser Gln Ala Ser Asn Gln Glu Lys Pro Leu Lys Glu Asp Ala Lys						
		85		90		95
Ala Val Thr Asn Glu Glu Val Asn Gln Met Ile Glu Asp Arg Lys Val		100		105		110
Asp Phe Asn Gln Asn Trp Tyr Phe Lys Leu Asn Ala Asn Ser Lys Glu		115		120		125
Ala Ile Lys Pro Asp Ala Asp Val Ser Thr Trp Lys Lys Leu Asp Leu		130		135		140
Pro Tyr Asp Trp Ser Ile Phe Asn Asp Phe Asp His Glu Ser Pro Ala			150		155	160
Gln Asn Glu Gly Gly Gln Leu Asn Gly Gly Glu Ala Trp Tyr Arg Lys		165		170		175
Thr Phe Lys Leu Asp Glu Lys Asp Leu Lys Lys Asn Val Arg Leu Thr		180		185		190
Phe Asp Gly Val Tyr Met Asp Ser Gln Val Tyr Val Asn Gly Gln Leu		195		200		205
Val Gly His Tyr Pro Asn Gly Tyr Asn Gln Phe Ser Tyr Asp Ile Thr		210		215		220
Lys Tyr Leu Gln Lys Asp Gly Arg Glu Asn Val Ile Ala Val His Ala		225		230		235
Val Asn Lys Gln Pro Ser Ser Arg Trp Tyr Ser Gly Ser Gly Ile Tyr		245		250		255
Arg Asp Val Thr Leu Gln Val Thr Asp Lys Val His Val Glu Lys Asn		260		265		270
Gly Thr Thr Ile Leu Thr Pro Lys Leu Glu Glu Gln Gln His Gly Lys		275		280		285
Val Glu Thr His Val Thr Ser Lys Ile Val Asn Thr Asp Asp Lys Asp		290		295		300
His Glu Leu Val Ala Glu Tyr Gln Ile Val Glu Arg Gly Gly His Ala		305		310		315
Val Thr Gly Leu Val Arg Thr Ala Ser Arg Thr Leu Lys Ala His Glu		325		330		335
Ser Thr Ser Leu Asp Ala Ile Leu Glu Val Glu Arg Pro Lys Leu Trp		340		345		350
Thr Val Leu Asn Asp Lys Pro Ala Leu Tyr Glu Leu Ile Thr Arg Val		355		360		365
Tyr Arg Asp Gly Gln Leu Val Asp Ala Lys Lys Asp Leu Phe Gly Tyr		370		375		380
Arg Tyr Tyr His Trp Thr Pro Asn Glu Gly Phe Ser Leu Asn Gly Glu		385		390		395
						400
Arg Ile Lys Phe His Gly Val Ser Leu His His Asp His Gly Ala Leu						

405										410					415									
Gly	Ala	Glu	Glu	Asn	Tyr	Lys	Ala	Glu	Tyr	Arg	Arg	Leu	Lys	Gln	Met									
420										425					430									
Lys	Glu	Met	Gly	Val	Asn	Ser	Ile	Arg	Thr	Thr	His	Asn	Pro	Ala	Ser									
435										440					445									
Glu	Gln	Thr	Leu	Gln	Ile	Ala	Ala	Glu	Leu	Gly	Leu	Leu	Val	Gln	Glu									
450										455					460									
Glu	Ala	Phe	Asp	Thr	Trp	Tyr	Gly	Gly	Lys	Lys	Pro	Tyr	Asp	Tyr	Gly									
465										470					475					480				
Arg	Phe	Phe	Glu	Lys	Asp	Ala	Thr	His	Pro	Glu	Ala	Arg	Lys	Gly	Glu									
485										490					495									
Lys	Trp	Ser	Asp	Phe	Asp	Leu	Arg	Thr	Met	Val	Glu	Arg	Gly	Lys	Asn									
500										505					510									
Asn	Pro	Ala	Ile	Phe	Met	Trp	Ser	Ile	Gly	Asn	Glu	Ile	Gly	Glu	Ala									
515										520					525									
Asn	Gly	Asp	Ala	His	Ser	Leu	Ala	Thr	Val	Lys	Arg	Leu	Val	Lys	Val									
530										535					540									
Ile	Lys	Asp	Val	Asp	Lys	Thr	Arg	Tyr	Val	Thr	Met	Gly	Ala	Asp	Lys									
545										550					555					560				
Phe	Arg	Phe	Gly	Asn	Gly	Ser	Gly	Gly	His	Glu	Lys	Ile	Ala	Asp	Glu									
565										570					575									
Leu	Asp	Ala	Val	Gly	Phe	Asn	Tyr	Ser	Glu	Asp	Asn	Tyr	Lys	Ala	Leu									
580										585					590									
Arg	Ala	Lys	His	Pro	Lys	Trp	Leu	Ile	Tyr	Gly	Ser	Glu	Thr	Ser	Ser									
595										600					605									
Ala	Thr	Arg	Thr	Arg	Gly	Ser	Tyr	Tyr	Arg	Pro	Glu	Arg	Glu	Leu	Lys									
610										615					620									
His	Ser	Asn	Gly	Pro	Glu	Arg	Asn	Tyr	Glu	Gln	Ser	Asp	Tyr	Gly	Asn									
625										630					635					640				
Asp	Arg	Val	Gly	Trp	Gly	Lys	Thr	Ala	Thr	Ala	Ser	Trp	Thr	Phe	Asp									
645										650					655									
Arg	Asp	Asn	Ala	Gly	Tyr	Ala	Gly	Gln	Phe	Ile	Trp	Thr	Gly	Thr	Asp									
660										665					670									
Tyr	Ile	Gly	Glu	Pro	Thr	Pro	Trp	His	Asn	Gln	Asn	Gln	Thr	Pro	Val									
675										680					685									
Lys	Ser	Ser	Tyr	Phe	Gly	Ile	Val	Asp	Thr	Ala	Gly	Ile	Pro	Lys	His									
690										695					700									
Asp	Phe	Tyr	Leu	Tyr	Gln	Ser																		
705										710														

(2) INFORMATION FOR SEQ ID NO: 83: -----

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2167 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTACTTTGGT ATCGTAGATA CAGCCGGCAT TCCAAAACAT GACTTCTATC TCTACCAAAG	60
CCAATGGGTT TCTGTTAAGA AGAAACCGAT GGTACACCTT CTTCTCACT GGAAGTGGGA	120
AAACAAAGAA TTAGCATCCA AAGTAGCTGA CTCAGAAGGT AAGATTCCAG TTCGTGCTTA	180
TTCGAATGCT TCTAGTGTAG AATTGTTCTT GAATGGAAAA TCTCTTGGTC TTAAGACTTT	240
CAATAAAAAA CAAACCAGCG ATGGGCGGAC TTACCAAGAA GGTGCAAATG CTAATGAACT	300
TTATCTTGAA TGGAAAGTTG CCTATCAACC AGGTACCTTG GAAGCAATTG CTCGTGATGA	360
ATCTGGCAAG GAAATTGCTC GAGATAAGAT TACGACTGCT GGTAAGCCAG CGGCAGTTCG	420
TCTTATTAAG GAAGACCATG CGATTGCAGC AGATGGAAAA GACTTGACTT ACATCTACTA	480
TGAAATTGTT GACAGCCAGG GGAATGTGGT TCCAAC TGCT AATAATCTGG TTCGCTTCCA	540
ATTGCATGGC CAAGGTCAAC TGGTCGGTGT AGATAACGGA GAACAAGCCA GCCGTGAACG	600
CTATAAGGCG CAAGCAGATG GTTCTTGGAT TCGTAAAGCA TTTAATGGTA AAGGTGTTGC	660
CATTGTCAAA TCAACTGAAC AAGCAGGGAA ATTCACCCTG ACTGCCCCACT CTGATCTCTT	720
GAAATCGAAC CAAGTCACTG TCTTTACTGG TAAGAAAGAA GGACAAGAGA AGACTGTTTT	780
GGGGACAGAA GTGCCAAAAG TACAGACCAT TATTGGAGAG GCACCTGAAA TGCCTACCAC	840
TGTTCCGTTT GTATACAGTG ATGGTAGCCG TGCAGAACGT CCTGTAACCT GGTCTTCAGT	900
AGATGTGAGC AAGCCTGGTA TTGTAACGGT GAAAGGTATG GCTGACGGAC GAGAAGTAGA	960
AGCTCGTGTA GAAGTGATTG CTCTTAAATC AGAGCTACCA GTTGTGAAAC GTATTGCTCC	1020
AAATACTGAC TTGAATTCTG TAGACAAATC TGTTTCCTAT GTTTTGATTG ATGGAAGTGT	1080
TGAAGAGTAT GAAGTGGACA AGTGGGAGAT TGCCGAAGAA GATAAAGCTA AGTTAGCAAT	1140
TCCAGGTTCT CGTATTCAAG CGACCGGTTA TTTAGAAGGT CAACCAATTC ATGCAACCCT	1200
TGTGGTAGAA GAAGGCAATC CTGCGGCACC TGCAGTACCA ACTGTAACGG TTGGTGGTGA	1260
GGCAGTAACA GGTCTTACTA GTCAAAAACC AATGCAATAC CGCACTCTTG CTTATGGAGC	1320
TAAGTTGCCA GAAGTCACAG CAAGTGCTAA AAATGCAGCT GTTACAGTTC TTCAAGCAAG	1380
CGCAGCAAAC GGCATGCGTG CGAGCATCTT TATTCAGCCT AAAGATGGTG GCCCTCTTCA	1440
AACCTATGCA ATTCAATTCC TTGAAGAAGC GCCAAAAATT GCTCACTTGA GCTTGCAAGT	1500
GGAAAAAGCT GACAGTCTCA AAGAAGACCA AACTGTCAAA TTGTCGGTTC GAGCTCACTA	1560
TCAAGATGGA ACGCAAGCTG TATTACCAGC TGATAAAGTA ACCTTCTCTA CAAGTGGTGA	1620
AGGGGAAGTC GCAATTCGTA AAGGAATGCT TGAGTTGCAT AAGCCAGGAG CAGTCACTCT	1680

GAACGCTGAA TATGAGGGAG CTAAAGACCA AGTTGAACTC ACTATCCAAG CCAATACTGA 1740
 GAAGAAGATT GCGCAATCCA TCCGTCCTGT AAATGTAGTG ACAGATTTGC ATCAGGAACC 1800
 AAGTCTTCCA GCAACAGTAA CAGTTGAGTA TGACAAAGGT TTCCCTAAAA CTCATAAAGT 1860
 CACTTGGCAA GCTATTCGGA AAGAAAAACT AGACTCCTAT CAAACATTTG AAGTACTAGG 1920
 TAAAGTTGAA GGAATTGACC TTGAAGCGCG TGCAAAAGTC TCTGTAGAAG GTATCGTTTC 1980
 AGTTGAAGAA GTCAGTGTGA CAACTCCAAT CGCAGAAGCA CCACAATTAC CAGAAAGTGT 2040
 TCGGACATAT GATTCAAATG GTCACGTTTC ATCAGCTAAG GTTGCATGGG ATGCGATTCTG 2100
 TCCAGAGCAA TACGCTAAGG AAGGTGTCTT TACAGTTAAT GGTCGCTTAG AAGGTACGCA 2160
 ATTAACA 2167

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His Asp Phe Tyr
 1 5 10 15
 Leu Tyr Gln Ser Gln Trp Val Ser Val Lys Lys Lys Pro Met Val His
 20 25 30
 Leu Leu Pro His Trp Asn Trp Glu Asn Lys Glu Leu Ala Ser Lys Val
 35 40 45
 Ala Asp Ser Glu Gly Lys Ile Pro Val Arg Ala Tyr Ser Asn Ala Ser
 50 55 60
 Ser Val Glu Leu Phe Leu Asn Gly Lys Ser Leu Gly Leu Lys Thr Phe
 65 70 75 80
 Asn Lys Lys Gln Thr Ser Asp Gly Arg Thr Tyr Gln Glu Gly Ala Asn
 85 90 95
 Ala Asn Glu Leu Tyr Leu Glu Trp Lys Val Ala Tyr Gln Pro Gly Thr
 100 105 110
 Leu Glu Ala Ile Ala Arg Asp Glu Ser Gly Lys Glu Ile Ala Arg Asp
 115 120 125
 Lys Ile Thr Thr Ala Gly Lys Pro Ala Ala Val Arg Leu Ile Lys Glu
 130 135 140
 Asp His Ala Ile Ala Ala Asp Gly Lys Asp Leu Thr Tyr Ile Tyr Tyr
 145 150 155 160
 Glu Ile Val Asp Ser Gln Gly Asn Val Val Pro Thr Ala Asn Asn Leu

165										170					175				
Val	Arg	Phe	Gln	Leu	His	Gly	Gln	Gly	Gln	Leu	Val	Gly	Val	Asp	Asn				
			180					185						190					
Gly	Glu	Gln	Ala	Ser	Arg	Glu	Arg	Tyr	Lys	Ala	Gln	Ala	Asp	Gly	Ser				
		195					200					205							
Trp	Ile	Arg	Lys	Ala	Phe	Asn	Gly	Lys	Gly	Val	Ala	Ile	Val	Lys	Ser				
	210					215					220								
Thr	Glu	Gln	Ala	Gly	Lys	Phe	Thr	Leu	Thr	Ala	His	Ser	Asp	Leu	Leu				
225					230					235					240				
Lys	Ser	Asn	Gln	Val	Thr	Val	Phe	Thr	Gly	Lys	Lys	Glu	Gly	Gln	Glu				
			245						250					255					
Lys	Thr	Val	Leu	Gly	Thr	Glu	Val	Pro	Lys	Val	Gln	Thr	Ile	Ile	Gly				
		260						265						270					
Glu	Ala	Pro	Glu	Met	Pro	Thr	Thr	Val	Pro	Phe	Val	Tyr	Ser	Asp	Gly				
		275					280					285							
Ser	Arg	Ala	Glu	Arg	Pro	Val	Thr	Trp	Ser	Ser	Val	Asp	Val	Ser	Lys				
	290					295					300								
Pro	Gly	Ile	Val	Thr	Val	Lys	Gly	Met	Ala	Asp	Gly	Arg	Glu	Val	Glu				
305					310					315					320				
Ala	Arg	Val	Glu	Val	Ile	Ala	Leu	Lys	Ser	Glu	Leu	Pro	Val	Val	Lys				
			325						330					335					
Arg	Ile	Ala	Pro	Asn	Thr	Asp	Leu	Asn	Ser	Val	Asp	Lys	Ser	Val	Ser				
		340						345						350					
Tyr	Val	Leu	Ile	Asp	Gly	Ser	Val	Glu	Glu	Tyr	Glu	Val	Asp	Lys	Trp				
	355						360					365							
Glu	Ile	Ala	Glu	Glu	Asp	Lys	Ala	Lys	Leu	Ala	Ile	Pro	Gly	Ser	Arg				
370					375						380								
Ile	Gln	Ala	Thr	Gly	Tyr	Leu	Glu	Gly	Gln	Pro	Ile	His	Ala	Thr	Leu				
385					390					395					400				
Val	Val	Glu	Glu	Gly	Asn	Pro	Ala	Ala	Pro	Ala	Val	Pro	Thr	Val	Thr				
			405						410					415					
Val	Gly	Gly	Glu	Ala	Val	Thr	Gly	Leu	Thr	Ser	Gln	Lys	Pro	Met	Gln				
		420					425						430						
Tyr	Arg	Thr	Leu	Ala	Tyr	Gly	Ala	Lys	Leu	Pro	Glu	Val	Thr	Ala	Ser				
	435					440					445								
Ala	Lys	Asn	Ala	Ala	Val	Thr	Val	Leu	Gln	Ala	Ser	Ala	Ala	Asn	Gly				
	450					455					460								
Met	Arg	Ala	Ser	Ile	Phe	Ile	Gln	Pro	Lys	Asp	Gly	Gly	Pro	Leu	Gln				
465					470					475					480				
Thr	Tyr	Ala	Ile	Gln	Phe	Leu	Glu	Glu	Ala	Pro	Lys	Ile	Ala	His	Leu				
		485							490					495					
Ser	Leu	Gln	Val	Glu	Lys	Ala	Asp	Ser	Leu	Lys	Glu	Asp	Gln	Thr	Val				

202

500

505

510

Lys Leu Ser Val Arg Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu
515 520 525

Pro Ala Asp Lys Val Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala
530 535 540

Ile Arg Lys Gly Met Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu
545 550 555 560

Asn Ala Glu Tyr Glu Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln
565 570 575

Ala Asn Thr Glu Lys Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val
580 585 590

Val Thr Asp Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val
595 600 605

Glu Tyr Asp Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala
610 615 620

Ile Pro Lys Glu Lys Leu Asp Ser Tyr Gln Thr Phe Glu Val Leu Gly
625 630 635 640

Lys Val Glu Gly Ile Asp Leu Glu Ala Arg Ala Lys Val Ser Val Glu
645 650 655

Gly Ile Val Ser Val Glu Glu Val Ser Val Thr Thr Pro Ile Ala Glu
660 665 670

Ala Pro Gln Leu Pro Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His
675 680 685

Val Ser Ser Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr
690 695 700

Ala Lys Glu Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln
705 710 715 720

Leu Thr

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AGCTAAGGTT GCATGGGATG CGATTCGTCC AGAGCAATAC GCTAAGGAAG GTGTCTTTAC	60
AGTTAATGGT CGCTTAGAAG GTACGCAATT AACAACTAAA CTTTCATGTTT GCGTATCTGC	120
TCAAAGTGAG CAAGGTGCAA ACATTTCTGA CCAATGGACC GGTTCAGAAT TGCCACTTGC	180
CTTTGCTTCA GACTCAAATC CAAGCGACCC AGTTTCAAAT GTTAATGACA AGCTCATTTT	240

CTACAATAAC CAACCAGCCA ATCGTTGGAC AAACCTGGAAT CGTACTAATC CAGAAGCTTC	300
AGTCGGTGTT CTGTTTGGAG ATTCAGGTAT CTTGAGCAAA CGCTCCGTTG ATAATCTAAG	360
TGTCGGATTC CATGAAGACC ATGGAGTTGG TGTACCGAAG TCTTATGTGA TTGAGTATTA	420
TGTTGGTAAG ACTGTCCCAA CAGCTCCTAA AAACCCTAGT TTTGTTGGTA ATGAGGACCA	480
TGTCTTTAAT GATTCTGCCA ACTGGAAACC AGTTACTAAT CTAAAAGCCC CTGCTCAACT	540
CAAGGCTGGA GAAATGAACC ACTTTAGCTT TGATAAAGTT GAAACCTATG CTGTTCTGAT	600
TCGCATGGTT AAAGCAGATA ACAAGCGTGG AACGTCTATC ACAGAGGTAC AAATCTTTGC	660
GAAACAAGTT GCGGCAGCCA AGCAAGGACA AACAAGAATC CAAGTTGACG GCAAAGACTT	720
AGCAAACCTC AACCCGTGATT TGACAGACTA CTACCTTGAG TCTGTAGATG GAAAAGTTCC	780
GGCAGTCACA GCAAGTGTTA GCAACAATGG TCTCGCTACC GTCGTTCCAA GCGTTCGTGA	840
AGGTGAGCCA GTTCGTGTCA TCGCGAAAGC TGAAAATGGC GACATCTTAG GAGAATACCG	900
TCTGCACTTC ACTAAGGATA AGAGCTTACT TTCTCATAAA CCAGTTGCTG CGGTAAACA	960
AGCTCGCTTG CTACAAGTAG GTCAAGCACT TGAATTGCCG ACTAAGGTTC CAGTTTACTT	1020
CACAGGTAAA GACGGCTACG AAACAAAAGA CCTGACAGTT GAATGGGAAG AAGTTCCAGC	1080
GGAAAATCTG ACAAAGCAG GTCAATTTAC TGTTCGAGGC CGTGTCCCTG GTAGTAACCT	1140
TGTTGCTGAG ATCACTGTAC GAGTGACAGA CAAACTTGGT GAGACTCTTT CAGATAACCC	1200
TAATATGAT GAAAACAGTA ACCAGGCCTT TGCTTCAGCA ACCAATGATA TTGACAAAAA	1260
CTCTCATGAC CGCGTTGACT ATCTCAATGA CGGAGATCAT TCAGAAAATC GTCGTTGGAC	1320
AAACTGGTCA CCAACACCAT CTTCTAATCC AGAAGTATCA GCGGGTGTGA TTTTCCGTGA	1380
AAATGGTAAG ATTGTAGAAC GGACTGTTAC ACAAGGAAAA GTTCAGTTCT TTGCAGATAG	1440
TGGTACGGAT GCACCATCTA AACTCGTTTT AGAACGCTAT GTCGGTCCAG AGTTTGAAGT	1500
GCCAACCTAC TATTCAAACCT ACCAAGCCTA CGACGCAGAC CATCCATTCA ACAATCCAGA	1560
AAATTGGGAA GCTGTTCCCTT ATCGTGCGGA TAAAGACATT GCAGCTGGTG ATGAAATCAA	1620
CGTAACATTT AAAGCTATCA AAGCCAAAGC TATGAGATGG CGTATGGAGC GTAAAGCAGA	1680
TAAGAGCGGT GTTGCGATGA TTGAGATGAC CTTCCCTTGCA CCAAGTGAAT TGCCTCAAGA	1740
AAGCACTCAA TCAAAGATTC TTGTAGATGG AAAAGAACTT GCTGATTTCTG CTGAAAATCG	1800
TCAAGACTAT CAAATTACCT ATAAAGGTCA ACGGCCAAAA GTCTCAGTTG AAGAAAACAA	1860
TCAAGTAGCT TCAACTGTGG TAGATAGTGG AGAAGATAGC TTTCCAGTAC TTGTTTCGCTT	1920
CGTTTCAGAA AGTGGAAC AAGTCAAGGA ATACCGTATC CACTTGACTA AGGAAAAACC	1980
AGTTTCTGAG AAGACAGTTG CTGCTGTACA AGAAGATCTT CAAAAATCG AATTTGTTGA	2040
AAAAGATTTG GCATACAAGA CAGTTGAGAA AAAAGATTCA AACTGTATC TAGGTGAAAC	2100

TCGTGTAGAA CAAGAAGGAA AAGTTGGAAA AGAACGTATC TTTACAGCGA TTAATCCTGA 2160
 TGGAAGTAAG GAAGAAAAAC TCCGTGAAGT GGTAGAAGTT CCGACAGACC GCATCGTCTT 2220
 GGTGGAACC AAACCAGTAG CTCAAGAAGC TAAAAACCA CAAGTGTCTAG AAAAAGCAGA 2280
 TACAAAACCA ATTGATTCAA GTGAAGCTAG TCAAATAAT AAAGCCCAG 2329

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr Ala Lys Glu
 1 5 10 15
 Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln Leu Thr Thr
 20 25 30
 Lys Leu His Val Arg Val Ser Ala Gln Thr Glu Gln Gly Ala Asn Ile
 35 40 45
 Ser Asp Gln Trp Thr Gly Ser Glu Leu Pro Leu Ala Phe Ala Ser Asp
 50 55 60
 Ser Asn Pro Ser Asp Pro Val Ser Asn Val Asn Asp Lys Leu Ile Ser
 65 70 75 80
 Tyr Asn Asn Gln Pro Ala Asn Arg Trp Thr Asn Trp Asn Arg Thr Asn
 85 90 95
 Pro Glu Ala Ser Val Gly Val Leu Phe Gly Asp Ser Gly Ile Leu Ser
 100 105 110
 Lys Arg Ser Val Asp Asn Leu Ser Val Gly Phe His Glu Asp His Gly
 115 120 125
 Val Gly Val Pro Lys Ser Tyr Val Ile Glu Tyr Tyr Val Gly Lys Thr
 130 135 140
 Val Pro Thr Ala Pro Lys Asn Pro Ser Phe Val Gly Asn Glu Asp His
 145 150 155 160
 Val Phe Asn Asp Ser Ala Asn Trp Lys Pro Val Thr Asn Leu Lys Ala
 165 170 175
 Pro Ala Gln Leu Lys Ala Gly Glu Met Asn His Phe Ser Phe Asp Lys
 180 185 190
 Val Glu Thr Tyr Ala Val Arg Ile Arg Met Val Lys Ala Asp Asn Lys
 195 200 205
 Arg Gly Thr Ser Ile Thr Glu Val Gln Ile Phe Ala Lys Gln Val Ala
 210 215 220

Ala	Ala	Lys	Gln	Gly	230		Thr	Arg	Ile	Gln	Val	Asp	Gly	Lys	Asp	Leu
225										235						240
Ala	Asn	Phe	Asn	Pro	Asp	Leu	Thr	Asp	Tyr	Tyr	Leu	Glu	Ser	Val	Asp	
				245					250					255		
Gly	Lys	Val	Pro	Ala	Val	Thr	Ala	Ser	Val	Ser	Asn	Asn	Gly	Leu	Ala	
			260					265					270			
Thr	Val	Val	Pro	Ser	Val	Arg	Glu	Gly	Glu	Pro	Val	Arg	Val	Ile	Ala	
		275					280					285				
Lys	Ala	Glu	Asn	Gly	Asp	Ile	Leu	Gly	Glu	Tyr	Arg	Leu	His	Phe	Thr	
	290					295					300					
Lys	Asp	Lys	Ser	Leu	Leu	Ser	His	Lys	Pro	Val	Ala	Ala	Val	Lys	Gln	
305					310					315					320	
Ala	Arg	Leu	Leu	Gln	Val	Gly	Gln	Ala	Leu	Glu	Leu	Pro	Thr	Lys	Val	
				325					330					335		
Pro	Val	Tyr	Phe	Thr	Gly	Lys	Asp	Gly	Tyr	Glu	Thr	Lys	Asp	Leu	Thr	
			340					345					350			
Val	Glu	Trp	Glu	Glu	Val	Pro	Ala	Glu	Asn	Leu	Thr	Lys	Ala	Gly	Gln	
		355					360					365				
Phe	Thr	Val	Arg	Gly	Arg	Val	Leu	Gly	Ser	Asn	Leu	Val	Ala	Glu	Ile	
	370					375					380					
Thr	Val	Arg	Val	Thr	Asp	Lys	Leu	Gly	Glu	Thr	Leu	Ser	Asp	Asn	Pro	
385					390					395					400	
Asn	Tyr	Asp	Glu	Asn	Ser	Asn	Gln	Ala	Phe	Ala	Ser	Ala	Thr	Asn	Asp	
				405					410					415		
Ile	Asp	Lys	Asn	Ser	His	Asp	Arg	Val	Asp	Tyr	Leu	Asn	Asp	Gly	Asp	
			420					425					430			
His	Ser	Glu	Asn	Arg	Arg	Trp	Thr	Asn	Trp	Ser	Pro	Thr	Pro	Ser	Ser	
		435					440					445				
Asn	Pro	Glu	Val	Ser	Ala	Gly	Val	Ile	Phe	Arg	Glu	Asn	Gly	Lys	Ile	
	450					455					460					
Val	Glu	Arg	Thr	Val	Thr	Gln	Gly	Lys	Val	Gln	Phe	Phe	Ala	Asp	Ser	
465					470					475					480	
Gly	Thr	Asp	Ala	Pro	Ser	Lys	Leu	Val	Leu	Glu	Arg	Tyr	Val	Gly	Pro	
				485					490					495		
Glu	Phe	Glu	Val	Pro	Thr	Tyr	Tyr	Ser	Asn	Tyr	Gln	Ala	Tyr	Asp	Ala	
			500					505					510			
Asp	His	Pro	Phe	Asn	Asn	Pro	Glu	Asn	Trp	Glu	Ala	Val	Pro	Tyr	Arg	
		515					520					525				
Ala	Asp	Lys	Asp	Ile	Ala	Ala	Gly	Asp	Glu	Ile	Asn	Val	Thr	Phe	Lys	
	530					535					540					
Ala	Ile	Lys	Ala	Lys	Ala	Met	Arg	Trp	Arg	Met	Glu	Arg	Lys	Ala	Asp	
545					550					555					560	

Lys Ser Gly Val Ala Met Ile Glu Met Thr Phe Leu Ala Pro Ser Glu
 565 570 575
 Leu Pro Gln Glu Ser Thr Gln Ser Lys Ile Leu Val Asp Gly Lys Glu
 580 585 590
 Leu Ala Asp Phe Ala Glu Asn Arg Gln Asp Tyr Gln Ile Thr Tyr Lys
 595 600 605
 Gly Gln Arg Pro Lys Val Ser Val Glu Glu Asn Asn Gln Val Ala Ser
 610 615 620
 Thr Val Val Asp Ser Gly Glu Asp Ser Phe Pro Val Leu Val Arg Leu
 625 630 635 640
 Val Ser Glu Ser Gly Lys Gln Val Lys Glu Tyr Arg Ile His Leu Thr
 645 650 655
 Lys Glu Lys Pro Val Ser Glu Lys Thr Val Ala Ala Val Gln Glu Asp
 660 665 670
 Leu Pro Lys Ile Glu Phe Val Glu Lys Asp Leu Ala Tyr Lys Thr Val
 675 680 685
 Glu Lys Lys Asp Ser Thr Leu Tyr Leu Gly Glu Thr Arg Val Glu Gln
 690 695 700
 Glu Gly Lys Val Gly Lys Glu Arg Ile Phe Thr Ala Ile Asn Pro Asp
 705 710 715 720
 Gly Ser Lys Glu Glu Lys Leu Arg Glu Val Val Glu Val Pro Thr Asp
 725 730 735
 Arg Ile Val Leu Val Gly Thr Lys Pro Val Ala Gln Glu Ala Lys Lys
 740 745 750
 Pro Gln Val Ser Glu Lys Ala Asp Thr Lys Pro Ile Asp Ser Ser Glu
 755 760 765
 Ala Ser Gln Thr Asn Lys Ala Gln
 770 775

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTATCACTAT GTAAATAAAG AGATTATTTT ACAAGAAGCT AAAGATTTAA TTCAGACAGG 60
 AAAGCCTGAC AGGAATGAAG TTGTATATGG TTTGGTGTAT CAAAAAGATC AGTTGCCTCA 120
 AACAGGGACA GAA 133

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Tyr His Tyr Val Asn Lys Glu Ile Ile Ser Gln Glu Ala Lys Asp Leu
1           5           10           15

Ile Gln Thr Gly Lys Pro Asp Arg Asn Glu Val Val Tyr Gly Leu Val
          20           25           30

Tyr Gln Lys Asp Gln Leu Pro Gln Thr Gly Thr Glu
          35           40

```

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 775 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

TGAGACTCCT CAATCAATAA CAAATCAGGA GCAAGCTAGG ACAGAAAACC AAGTAGTAGA      60
GACAGAGGAA GCTCCAAAAG AAGAAGCACC TAAACAGAA GAAAGTCCAA AGGAAGAACC      120
AAAATCGGAG GTAAACCTA CTGACGACAC CCTTCCTAAA GTAGAAGAGG GGAAAGAAGA      180
TTCAGCAGAA CCAGCTCCAG TTGAAGAAGT AGGTGGAGAA GTTGAGTCAA AACCAGAGGA      240
AAAAGTAGCA GTTAAGCCAG AAAGTCAACC ATCAGACAAA CCAGCTGAGG AATCAAAAAGT      300
TGAACAAGCA GGTGAACCAG TCGCGCCAAG AGAAGACGAA AAGGCACCAG TCGAGCCAGA      360
AAAGCAACCA GAAGCTCCTG AAGAAGAGAA GGCTGTAGAG GAAACACCGA AACAAGAAGA      420
GTCAACTCCA GATACCAAGG CTGAAGAAAC TGTAGAACCA AAAGAGGAGA CTGTTAATCA      480
ATCTATTGAA CAACCAAAAG TTGAAACGCC TGCTGTAGAA AAACAAACAG AACCAACAGA      540
GGAACCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AACAGGCACC      600
AACGGCACCA GTTGAGCCAG AAAAGCAACC AGAAGTTCCT GAAGAAGAGA AGGCTGTAGA      660
GGAAACACCG AAACCAGAAG ATAAAATAAA GGGTATTGGT ACTAAAGAAC CAGTTGATAA      720
AAGTGAGTTA AATAATCAAA TTGATAAAGC TAGTTCAGTT TCTCCTACTG ATTAT      775

```

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala Arg Thr Glu Asn
 1 5 10 15
 Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu Ala Pro Lys Thr
 20 25 30
 Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val Lys Pro Thr Asp
 35 40 45
 Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp Ser Ala Glu Pro
 50 55 60
 Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser Lys Pro Glu Glu
 65 70 75 80
 Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp Lys Pro Ala Glu
 85 90 95
 Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala Pro Arg Glu Asp
 100 105 110
 Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu Ala Pro Glu Glu
 115 120 125
 Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu Ser Thr Pro Asp
 130 135 140
 Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu Thr Val Asn Gln
 145 150 155 160
 Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val Glu Lys Gln Thr
 165 170 175
 Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly Glu Pro Val Ala
 180 185 190
 Pro Arg Glu Asp Glu Gln Ala Pro Thr Ala Pro Val Glu Pro Glu Lys
 195 200 205
 Gln Pro Glu Val Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys
 210 215 220
 Pro Glu Asp Lys Ile Lys Gly Ile Gly Thr Lys Glu Pro Val Asp Lys
 225 230 235 240
 Ser Glu Leu Asn Asn Gln Ile Asp Lys Ala Ser Ser Val Ser Pro Thr
 245 250 255
 Asp Tyr

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

GGATGCTCAA GAAACTGCGG GAGTTCAC TA AATATGTG GCAGATTCAG AGCTATCATC      60
AGAAGAAAAG AAGCAGCTTG TCTATGATAT TCCGACATAC GTGGAGAATG ATGATGAAAC      120
TTATTATCTT GTTTATAAGT TAAATTCTCA AAATCAACTG GCGGAATTGC CAAATACTGG      180
AAGCAAGAAT GAGAGGCAA                                                    199

```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Asp Ala Gln Glu Thr Ala Gly Val His Tyr Lys Tyr Val Ala Asp Ser
1           5           10           15

Glu Leu Ser Ser Glu Glu Lys Lys Gln Leu Val Tyr Asp Ile Pro Thr
          20           25           30

Tyr Val Glu Asn Asp Asp Glu Thr Tyr Tyr Leu Val Tyr Lys Leu Asn
          35           40           45

Ser Gln Asn Gln Leu Ala Glu Leu Pro Asn Thr Gly Ser Lys Asn Glu
          50           55           60

Arg Gln
65

```

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

CGACAAAGGT GAGACTGAGG TTCAACCAGA GTCGCCAGAT ACTGTGGTAA GTGATAAAGG      60
TGAACCAGAG CAGGTAGCAC CGCTTCCAGA ATATAAGGGT AATATTGAGC AAGTAAAC      120
TGAAACTCCG GTTGAAGAAG CCAAAGAACA AGGTCCAGAA AAAACTGAAG AAGTTCCAGT      180
AAAACCAACA GAAGAAACAC CAGTAAATCC AAATGAAGGT ACTACAGAAG GAACCTCAAT      240

```

TCAAGAAGCA GAAAATCCAG TTCAACCTGC AGAAGAATCA ACAACGAATT CAGAGAAAGT 300
 ATCACCAGAT ACATCTAGCA AAAATACTGG GGAAGTGTCC AGTAATCCTA GTGATTTCGAC 360
 AACCTCAGTT GGAGAATCAA ATAAACCAGA ACATAATGAC TCTAAAAATG AAAATTCAGA 420
 AAAAACTGTA GAAGAAGTTC CAGTAAATCC AAATGAAGGC ACAGTAGAAG GTACCTCAAA 480
 TCAAGAAACA GAAAAACCAG TTCAACCTGC AGAAGAAACA CAAACAAACT CTGGGAAAAAT 540
 AGCTAACGAA AATACTGGAG AAGTATCCAA TAAACCTAGT GATTCAAAAC CACCACTTGA 600
 AGAATCAAAT CAACCAGAAA AAAACGGAAC TGCAACAAAA CCAGAAAATT CAGGTAATAC 660
 AACATCAGAG AATGGACAAA CAGAACCAGA ACCATCAAAC GGAAATTCAA CTGAGGATGT 720
 TTCAACCGAA TCAAACACAT CCAATTCAAA TGGAAACGAA GAAATTAAAC AAGAAAATGA 780
 ACTAGACCCT GATAAAAAGG TAGAAGAACC AGAGAAAACA CTTGAATTAA GAAAT 835

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp	Lys	Gly	Glu	Thr	Glu	Val	Gln	Pro	Glu	Ser	Pro	Asp	Thr	Val	Val	1	5	10	15
Ser	Asp	Lys	Gly	Glu	Pro	Glu	Gln	Val	Ala	Pro	Leu	Pro	Glu	Tyr	Lys	20	25	30	
Gly	Asn	Ile	Glu	Gln	Val	Lys	Pro	Glu	Thr	Pro	Val	Glu	Lys	Thr	Lys	35	40	45	
Glu	Gln	Gly	Pro	Glu	Lys	Thr	Glu	Glu	Val	Pro	Val	Lys	Pro	Thr	Glu	50	55	60	
Glu	Thr	Pro	Val	Asn	Pro	Asn	Glu	Gly	Thr	Thr	Glu	Gly	Thr	Ser	Ile	65	70	75	80
Gln	Glu	Ala	Glu	Asn	Pro	Val	Gln	Pro	Ala	Glu	Glu	Ser	Thr	Thr	Asn	85	90	95	
Ser	Glu	Lys	Val	Ser	Pro	Asp	Thr	Ser	Ser	Lys	Asn	Thr	Gly	Glu	Val	100	105	110	
Ser	Ser	Asn	Pro	Ser	Asp	Ser	Thr	Thr	Ser	Val	Gly	Glu	Ser	Asn	Lys	115	120	125	
Pro	Glu	His	Asn	Asp	Ser	Lys	Asn	Glu	Asn	Ser	Glu	Lys	Thr	Val	Glu	130	135	140	
Glu	Val	Pro	Val	Asn	Pro	Asn	Glu	Gly	Thr	Val	Glu	Gly	Thr	Ser	Asn	145	150	155	160

Gln Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn
 165 170 175

Ser Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro
 180 185 190

Ser Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn
 195 200 205

Gly Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn
 210 215 220

Gly Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val
 225 230 235 240

Ser Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys
 245 250 255

Gln Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys
 260 265 270

Thr Leu Glu Leu Arg Asn
 275

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 709 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAATCAATTG GTAGCACAAG ATCCAAAAGC ACAAGATAGC ACTAAACTGA CTGCTGAAAA 60
 ATCAACTGTT AAAGCACCTG CTCAAAGAGT AGATGTAAAA GATATAACTC ATTTAACAGA 120
 TGAAGAAAAA GTTAAGGTTG CTATTTTACA AGCAAATGGT TCAGCATTAG ACGGAGCGAC 180
 AATCAATGTA GCTGGAGATG GTACAGCAAC AATCACATTC CCAGATGGTT CAGTAGTGAC 240
 GATTCTAGGA AAAGATACAG TTCAACAATC TGCGAAAGGT GAATCTGTAA CTCAAGAAGC 300
 TACACCAGAG TATAAGCTAG AAAATACACC AGGTGGAGAT AAGGGAGGCA ATACTGGAAG 360
 CTCAGATGCT AATGCGAATG AAGGCGGTGG TAGCCAGGCG GGTGGATCAG CTCACACAGG 420
 TTCACAAAAC TCAGCTCAAT CACAAGCTTC TAAGCAATTA GCTACTGAAA AAGAATCAGC 480
 TAAAAATGCC ATTGAAAAAG CAGCCAAGGA CAAGCAGGAT GAAATCAAAG GCGCACCCT 540
 TTCTGATAAA GAAAAAGCAG AACTTTTAGC AAGAGTGGAA GCAGAAAAAC AAGCAGCTCT 600
 CAAAGAGATT GAAATGCGA AACTATGGA AGATGTGAAG GAAGCAGAAA CGATTGGAGT 660
 GCAAGCCATT GCCATGGTTA CAGTTCCTAA GAGACCAGTG GCTCCTAAT 709

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

Asn	Gln	Leu	Val	Ala	Gln	Asp	Pro	Lys	Ala	Gln	Asp	Ser	Thr	Lys	Leu
1			5						10					15	
Thr	Ala	Glu	Lys	Ser	Thr	Val	Lys	Ala	Pro	Ala	Gln	Arg	Val	Asp	Val
			20					25					30		
Lys	Asp	Ile	Thr	His	Leu	Thr	Asp	Glu	Glu	Lys	Val	Lys	Val	Ala	Ile
		35					40					45			
Leu	Gln	Ala	Asn	Gly	Ser	Ala	Leu	Asp	Gly	Ala	Thr	Ile	Asn	Val	Ala
	50					55					60				
Gly	Asp	Gly	Thr	Ala	Thr	Ile	Thr	Phe	Pro	Asp	Gly	Ser	Val	Val	Thr
65					70					75					80
Ile	Leu	Gly	Lys	Asp	Thr	Val	Gln	Gln	Ser	Ala	Lys	Gly	Glu	Ser	Val
			85					90						95	
Thr	Gln	Glu	Ala	Thr	Pro	Glu	Tyr	Lys	Leu	Glu	Asn	Thr	Pro	Gly	Gly
			100					105					110		
Asp	Lys	Gly	Gly	Asn	Thr	Gly	Ser	Ser	Asp	Ala	Asn	Ala	Asn	Glu	Gly
		115					120					125			
Gly	Gly	Ser	Gln	Ala	Gly	Gly	Ser	Ala	His	Thr	Gly	Ser	Gln	Asn	Ser
	130					135					140				
Ala	Gln	Ser	Gln	Ala	Ser	Lys	Gln	Leu	Ala	Thr	Glu	Lys	Glu	Ser	Ala
145					150					155					160
Lys	Asn	Ala	Ile	Glu	Lys	Ala	Ala	Lys	Asp	Lys	Gln	Asp	Glu	Ile	Lys
			165					170						175	
Gly	Ala	Pro	Leu	Ser	Asp	Lys	Glu	Lys	Ala	Glu	Leu	Leu	Ala	Arg	Val
			180					185					190		
Glu	Ala	Glu	Lys	Gln	Ala	Ala	Leu	Lys	Glu	Ile	Glu	Asn	Ala	Lys	Thr
		195					200					205			
Met	Glu	Asp	Val	Lys	Glu	Ala	Glu	Thr	Ile	Gly	Val	Gln	Ala	Ile	Ala
	210					215					220				
Met	Val	Thr	Val	Pro	Lys	Arg	Pro	Val	Ala	Pro	Asn				
225					230					235					

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CAAACAGTCA GCTTCAGGAA CGATTGAGGT GATTTACGA GAAAATGGCT CTGGGACACG 60
 GGGTGCCTTC ACAGAAATCA CAGGGATTCT CAAAAAGAC GGTGATAAAA AAATTGACAA 120
 CACTGCCAAA ACAGCTGTGA TTCAAATAG TACAGAAGGT GTTCTCTCAG CAGTTCAAGG 180
 GAATGCTAAT GCTATCGGCT ACATCTCCTT GGGATCTTTA ACGAAATCTG TCAAGGCTTT 240
 AGAGATTGAT GGTGTCAAGG CTAGTCGAGA CACAGTTTTA GATGGTGAAT ACCCTCTTCA 300
 ACGTCCCTTC AACATTGTTT GGTCTTCTAA TCTTTCCAAG CTAGGTCAAG ATTTTATCAG 360
 CTTTATCCAC TCCAAACAAG GTCAACAAGT GGTCACAGAT AATAAATTTA TTGAAGCTAA 420
 AACCGAAACC ACGGAATATA CAAGCCAACA CTTATCAGGC AAGTTGTCTG TTGTAGGTTT 480
 CACTTCAGTA TCTTCTTTAA TGGAAAAATT AGCAGAAGCT TATAAAAAAG AAAATCCAGA 540
 AGTTACGATT GATATTACCT CTAATGGGTC TTCAGCAGGT ATTACCGCTG TTAAGGAGAA 600
 AACCGCTGAT ATTGGTATGG TTTCTAGGGA ATTAATCCTT GAAGAAGGTA AGAGTCTCAC 660
 CCATGATGCT ATTGCTTTAG ACGGTATTGC TGTTGTGGTC AATAATGACA ATAAGGCAAG 720
 CCAAGTCAGT ATGGCTGAAC TTGCAGACGT TTTTAGTGGC AAATTAACCA CCTGGGACAA 780
 GATTAAA 787

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys Gln Ser Ala Ser Gly Thr Ile Glu Val Ile Ser Arg Glu Asn Gly
 1 5 10 15
 Ser Gly Thr Arg Gly Ala Phe Thr Glu Ile Thr Gly Ile Leu Lys Lys
 20 25 30
 Asp Gly Asp Lys Lys Ile Asp Asn Thr Ala Lys Thr Ala Val Ile Gln
 35 40 45
 Asn Ser Thr Glu Gly Val Leu Ser Ala Val Gln Gly Asn Ala Asn Ala
 50 55 60
 Ile Gly Tyr Ile Ser Leu Gly Ser Leu Thr Lys Ser Val Lys Ala Leu
 65 70 75 80
 Glu Ile Asp Gly Val Lys Ala Ser Arg Asp Thr Val Leu Asp Gly Glu
 85 90 95

214

Tyr Pro Leu Gln Arg Pro Phe Asn Ile Val Trp Ser Ser Asn Leu Ser
100 105 110

Lys Leu Gly Gln Asp Phe Ile Ser Phe Ile His Ser Lys Gln Gly Gln
115 120 125

Gln Val Val Thr Asp Asn Lys Phe Ile Glu Ala Lys Thr Glu Thr Thr
130 135 140

Glu Tyr Thr Ser Gln His Leu Ser Gly Lys Leu Ser Val Val Gly Ser
145 150 155 160

Thr Ser Val Ser Ser Leu Met Glu Lys Leu Ala Glu Ala Tyr Lys Lys
165 170 175

Glu Asn Pro Glu Val Thr Ile Asp Ile Thr Ser Asn Gly Ser Ser Ala
180 185 190

Gly Ile Thr Ala Val Lys Glu Lys Thr Ala Asp Ile Gly Met Val Ser
195 200 205

Arg Glu Leu Thr Pro Glu Glu Gly Lys Ser Leu Thr His Asp Ala Ile
210 215 220

Ala Leu Asp Gly Ile Ala Val Val Val Asn Asn Asp Asn Lys Ala Ser
225 230 235 240

Gln Val Ser Met Ala Glu Leu Ala Asp Val Phe Ser Gly Lys Leu Thr
245 250 255

Thr Trp Asp Lys Ile Lys
260

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATTCGATGAT GCGGATGAAA AGATGACCCG TGATGAAATT GCCTATATGC TGACAAATAG	60
TGAAGAAACA TTGGATGCTG ATGAGATTGA GATGCTACAA GGTGTCTTTT CGCTCGATGA	120
ACTGATGGCA CGAGAGGTTA TGGTTCCTCG AACGGATGCC TTTATGGTGG ATATTCAGGA	180
TGATAGTCAA GCCATTATCC AAAGTATTTT AAAACAAAAT TATTCTCGTA TCCCGGTTTA	240
TGATGGGGAT AAGGACAATG TAATTGGAAT CATTACACCC AAGAGTCTCC TTAAGGCAGG	300
CTTTGTGGAC GGTTTTGACA ATATTGTTTG GAAGAGAATT TTACAAGATC CACTTTTTGT	360
ACCTGAAACT ATTTTGTGG ATGACTTGCT AAAAGAACTG CGAAATACCC AAAGACAAAT	420
G	421

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Phe Asp Asp Ala Asp Glu Lys Met Thr Arg Asp Glu Ile Ala Tyr Met
1           5           10           15
Leu Thr Asn Ser Glu Glu Thr Leu Asp Ala Asp Glu Ile Glu Met Leu
20           25           30
Gln Gly Val Phe Ser Leu Asp Glu Leu Met Ala Arg Glu Val Met Val
35           40           45
Pro Arg Thr Asp Ala Phe Met Val Asp Ile Gln Asp Asp Ser Gln Ala
50           55           60
Ile Ile Gln Ser Ile Leu Lys Gln Asn Tyr Ser Arg Ile Pro Val Tyr
65           70           75           80
Asp Gly Asp Lys Asp Asn Val Ile Gly Ile Ile His Thr Lys Ser Leu
85           90           95
Leu Lys Ala Gly Phe Val Asp Gly Phe Asp Asn Ile Val Trp Lys Arg
100          105          110
Ile Leu Gln Asp Pro Leu Phe Val Pro Glu Thr Ile Phe Val Asp Asp
115          120          125
Leu Leu Lys Glu Leu Arg Asn Thr Gln Arg Gln Met
130          135          140

```

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

GGAGAGTCGA TCAAAAGTAG ATGAAGCTGT GTCTAAGTTT GAAAAGGACT CATCTTCTTC      60
GTCAAGTTCA GACTCTTCCA CTAAACCGGA AGCTTCAGAT ACAGCGAAGC CAAACAAGCC      120
GACAGAACCA GGAGAAAAGG TAGCAGAAGC TAAGAAGAAG GTTGAAGAAG CTGAGAAAAA      180
AGCCAAGGAT CAAAAAGAAG AAGATCGTCG TAACTACCCA ACCATTACTT ACAAACGCT      240
TGAAGTTGAA ATTGCTGAGT CCGATGTGGA AGTTAAAAAA GCGGAGCTTG AACTAGTAAA      300
AGTGAAAGCT AACGAACCTC GAGACGAGCA A                                331

```

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Glu Ser Arg Ser Lys Val Asp Glu Ala Val Ser Lys Phe Glu Lys Asp
1           5           10           15
Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Lys Pro Glu Ala Ser
          20           25           30
Asp Thr Ala Lys Pro Asn Lys Pro Thr Glu Pro Gly Glu Lys Val Ala
          35           40           45
Glu Ala Lys Lys Lys Val Glu Glu Ala Glu Lys Lys Ala Lys Asp Gln
          50           55           60
Lys Glu Glu Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys Thr Leu
65           70           75           80
Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu
          85           90           95
Glu Leu Val Lys Val Lys Ala Asn Glu Pro Arg Asp Glu Gln
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ATGGACAACA GGAAACTGGG ACGAGGTTAT ATCTGGTAAG ATTGACAAGT ACAAAGATCC      60
AGATATTCCA ACAGTTGAAT CACAAGAAGT TACGTCAGAC TCTAGTGATA AAGAAATAAC      120
GGTAAGGTAT GACCGTTTAT CAACACCAGA AAAACCAATC CCACAACCAA ATCCAGAGCA      180
TCCAAGTGTT CCGACACCAA ACCCAGAACT ACCAAATCAA GAGACTCCAA CACCAGATAA      240
ACCAACTCCA GAACCAGGTA CTCCAAAAAC TGAAACTCCA GTGAATCCAG ACCCAGAAGT      300
TCCGACTTAT GAGACAGGTA AGAGAGAGGA ATTGCCAAAC ACAGGTACAG AAGCTAAT      358

```

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

093331-1001
 102310-123360

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Trp	Thr	Thr	Gly	Asn	Trp	Asp	Glu	Val	Ile	Ser	Gly	Lys	Ile	Asp	Lys
1				5					10					15	
Tyr	Lys	Asp	Pro	Asp	Ile	Pro	Thr	Val	Glu	Ser	Gln	Glu	Val	Thr	Ser
			20					25					30		
Asp	Ser	Ser	Asp	Lys	Glu	Ile	Thr	Val	Arg	Tyr	Asp	Arg	Leu	Ser	Thr
		35					40					45			
Pro	Glu	Lys	Pro	Ile	Pro	Gln	Pro	Asn	Pro	Glu	His	Pro	Ser	Val	Pro
	50					55					60				
Thr	Pro	Asn	Pro	Glu	Leu	Pro	Asn	Gln	Glu	Thr	Pro	Thr	Pro	Asp	Lys
65					70					75					80
Pro	Thr	Pro	Glu	Pro	Gly	Thr	Pro	Lys	Thr	Glu	Thr	Pro	Val	Asn	Pro
				85					90					95	
Asp	Pro	Glu	Val	Pro	Thr	Tyr	Glu	Thr	Gly	Lys	Arg	Glu	Glu	Leu	Pro
			100					105						110	
Asn	Thr	Gly	Thr	Glu	Ala	Asn									
			115												

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CGATGGGCTC AATCCAACCC CAGGTCAAGT CTTACCTGAA GAGACATCGG GAACGAAAGA	60
GGGTGACTTA TCAGAAAAAC CAGGAGACAC CGTTCTCACT CAAGCGAAAC CTGAGGGCGT	120
TACTGGAAAT ACGAATTCAC TTCCGACACC TACAGAAAGA ACTGAAGTGA GCGAGGAAAC	180
AAGCCCTTCT AGTCTGGATA CACTTTTTGA AAAAGATGAA GAAGCTCAAA AAAATCCAGA	240
GCTAACAGAT GTCTTAAAAG AACTGTAGA TACAGCTGAT GTGGATGGGA CACAAGCAAG	300
TCCAGCAGAA ACTACTCCTG AACAAGTAAA AGGTGGAGTG AAAGAAAATA CAAAAGACAG	360
CATCGATGTT CCTGCTGCTT ATCTTGAAAA AGCTGAAGGG AAAGGTCCTT TCACTGCCGG	420
TGTAAACCAA GTAATTCCTT ATGAACATT CGCTGGTGAT GGTATGTTAA CTCGTCTATT	480
ACTAAAAGCT TCGGATAATG CTCCTTGGTC TGACAATGGT ACTGCTAAAA ATCCTGCTTT	540
ACCTCCTCTT GAAGGATTAA CAAAAGGGAA ATACTTCTAT GAAGTAGACT TAAATGGCAA	600

TACTGTTGGT AAACAAGGTC AAGCTTTAAT TGATCAACTT CGCGCTAATG GTACTCAAAC 660
 TTATAAAGCT ACTGTTAAAG TTTACGGAAA TAAAGACGGT AAAGCTGACT TGACTAATCT 720
 AGTTGCTACT AAAAATGTAG ACATCAACAT CAATGGATTA GTTGCTAAAG AAACAGTTCA 780
 AAAAGCCGTT GCAGACAACG TTAAAGACAG TATCGATGTT CCAGCAGCCT ACCTAGAAAA 840
 AGCCAAGGGT GAAGGTCCAT TCACAGCAGG TGTCAACCAT GTGATTCCAT ACGAACTCTT 900
 CGCAGGTGAT GGCATGTTGA CTCGTCTCTT GCTCAAGGCA TCTGACAAGG CACCATGGTC 960
 AGATAACGGC GACGCTAAAA ACCCAGCCCT ATCTCCACTA GCGGAAAACG TGAAGACCAA 1020
 AGGTCAATAC TTCTATCAAN TAGCCTTGGA CGGAAATGTA GCTGGCAAAG AAAAACAAGC 1080
 GCTCATTGAC CAGTTCCGAG CAAANGGTAC TCAAACCTAC AGCGCTACAG TCAATGTCTA 1140
 TGGTAACAAA GACGGTAAAC CAGACTTGGA CAACATCGTA GCAACTAAAA AAGTCACTAT 1200
 TAACATAAAC GGTTTAATTT CTAAAGAAAC AGTTCAAAAA GCCGTTGCAG ACAACGTTAA 1260
 NGACAGTATC GATGTTCCAG CAGCCTACCT AGAAAAAGCC AAGGGTGAAG GTCCATTAC 1320
 AGCAGGTGTC AACCATGTGA TTCCATACGA ACTCTTCGCA GGTGATGGTA TGTTGACTCG 1380
 TCTCTTGCTC AAGGCATCTG ACAAGGCACC ATGGTCAGAT AACGNGACG CTAAAAACCC 1440
 AGCNCTATCT CCACTAGGTG AAAACGTGAA GACCAAAGGT CAATACTTCT ATCAANTAGC 1500
 CTTGGACGGA AATGTAGCTG GCAAAGAAAA ACAAGCGCTC ATTGACCAGT TCCGAGCAAA 1560
 CGGTACTCAA ACTTACAGCG CTACAGTCAA TGTCTATGGT AACAAAGACG GTAAACCAGA 1620
 CTTGGACAAC ATCGTAGCAA CTAAAAAAGT CACTATTAAG ATAAATGTTA AAGAAACATC 1680
 AGACACAGCA AATGGTTCAT TATCACCTTC TAACTCTGGT TCTGGCGTGA CTCCGATGAA 1740
 TCACAATCAT GCTACAGGTA CTACAGATAG CATGCCTGCT GACACCATGA CAAGTTCTAC 1800
 CAACACGATG GCAGGTGAAA ACATGGCTGC TTCTGCTAAC AAGATGTCTG ATACGATGAT 1860
 GTCAGAGGAT AAAGCTATG 1879

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Asp Gly Leu Asn Pro Thr Pro Gly Gln Val Leu Pro Glu Glu Thr Ser
 1 5 10 15
 Gly Thr Lys Glu Gly Asp Leu Ser Glu Lys Pro Gly Asp Thr Val Leu
 20 25 30

Thr Gln Ala Lys Pro Glu Gly Val Thr Gly Asn Thr Asn Ser Leu Pro
 35 40 45
 Thr Pro Thr Glu Arg Thr Glu Val Ser Glu Glu Thr Ser Pro Ser Ser
 50 55 60
 Leu Asp Thr Leu Phe Glu Lys Asp Glu Glu Ala Gln Lys Asn Pro Glu
 65 70 75 80
 Leu Thr Asp Val Leu Lys Glu Thr Val Asp Thr Ala Asp Val Asp Gly
 85 90 95
 Thr Gln Ala Ser Pro Ala Glu Thr Thr Pro Glu Gln Val Lys Gly Gly
 100 105 110
 Val Lys Glu Asn Thr Lys Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu
 115 120 125
 Glu Lys Ala Glu Gly Lys Gly Pro Phe Thr Ala Gly Val Asn Gln Val
 130 135 140
 Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu
 145 150 155 160
 Leu Lys Ala Ser Asp Asn Ala Pro Trp Ser Asp Asn Gly Thr Ala Lys
 165 170 175
 Asn Pro Ala Leu Pro Pro Leu Glu Gly Leu Thr Lys Gly Lys Tyr Phe
 180 185 190
 Tyr Glu Val Asp Leu Asn Gly Asn Thr Val Gly Lys Gln Gly Gln Ala
 195 200 205
 Leu Ile Asp Gln Leu Arg Ala Asn Gly Thr Gln Thr Tyr Lys Ala Thr
 210 215 220
 Val Lys Val Tyr Gly Asn Lys Asp Gly Lys Ala Asp Leu Thr Asn Leu
 225 230 235 240
 Val Ala Thr Lys Asn Val Asp Ile Asn Ile Asn Gly Leu Val Ala Lys
 245 250 255
 Glu Thr Val Gln Lys Ala Val Ala Asp Asn Val Lys Asp Ser Ile Asp
 260 265 270
 Val Pro Ala Ala Tyr Leu Glu Lys Ala Lys Gly Glu Gly Pro Phe Thr
 275 280 285
 Ala Gly Val Asn His Val Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly
 290 295 300
 Met Leu Thr Arg Leu Leu Lys Ala Ser Asp Lys Ala Pro Trp Ser
 305 310 315 320
 Asp Asn Gly Asp Ala Lys Asn Pro Ala Leu Ser Pro Leu Gly Glu Asn
 325 330 335
 Val Lys Thr Lys Gly Gln Tyr Phe Tyr Gln Xaa Ala Leu Asp Gly Asn
 340 345 350
 Val Ala Gly Lys Glu Lys Gln Ala Leu Ile Asp Gln Phe Arg Ala Xaa
 355 360 365

Gly Thr Gln Thr Tyr Ser Ala Thr Val Asn Val Tyr Gly Asn Lys Asp
 370 375 380
 Gly Lys Pro Asp Leu Asp Asn Ile Val Ala Thr Lys Lys Val Thr Ile
 385 390 395 400
 Asn Ile Asn Gly Leu Ile Ser Lys Glu Thr Val Gln Lys Ala Val Ala
 405 410 415
 Asp Asn Val Xaa Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys
 420 425 430
 Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val Ile Pro
 435 440 445
 Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu Leu Lys
 450 455 460
 Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys Asn Pro
 465 470 475 480
 Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln Tyr Phe
 485 490 495
 Tyr Gln Xaa Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys Gln Ala
 500 505 510
 Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser Ala Thr
 515 520 525
 Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp Asn Ile
 530 535 540
 Val Ala Thr Lys Lys Val Thr Ile Lys Ile Asn Val Lys Glu Thr Ser
 545 550 555 560
 Asp Thr Ala Asn Gly Ser Leu Ser Pro Ser Asn Ser Gly Ser Gly Val
 565 570 575
 Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp Ser Met Pro
 580 585 590
 Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly Glu Asn Met
 595 600 605
 Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser Glu Asp Lys
 610 615 620
 Ala Met
 625

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

TTCCAATCAA AAACAGGCAG ATGGTAAACT CAATATCGTG ACAACCTTTT ACCCTGTCTA 60
 TGA rTTTACC AAGCAAGTCG CAGGAGATAC GGCTAATGTA GAACCTCTAA TCGGTGCTGG 120
 GACAGAACCT CATGAATACG AACCATCTGC CAAGGCAGTT GCCAAAATCC AAGATGCAGA 180
 TACCTTCGTT TATGAAAATG AAAACATGGA AACATGGGTA CCTAAATTGC TAGATACCTT 240
 GGATAAGAAA AAAGTGAAAA CCATCAAGGC GACAGGCGAT ATGTTGCTCT TGCCAGGTGG 300
 CGAGGAAGAA GAGGGAGACC ATGACCATGG AGAAGAAGGT CATCACCATG AGTTTGACCC 360
 CCATGTTTGG TTATCACCAG TTCGTGCCAT tAAACTAGTA GAGCACCATC CGCGACACTT 420
 GTCAGCAGAT TATCCTGATA AAAAAGAGAC CTTTGAGAAG AATGCAGCTG CCTATATCGA 480
 AAAATTGCAA GCCTTGGATA AGGCTTACGC AGAAGGTTTG TCTCAAGCAA AACAAAAGAG 540
 CTTTGTGACT CAACACGCag CCTTTAACTa TCTTGCCTTG GACTATGGGA CTC 593

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 197 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Ser	Asn	Gln	Lys	Gln	Ala	Asp	Gly	Lys	Leu	Asn	Ile	Val	Thr	Thr	Phe	1	5	10	15
Tyr	Pro	Val	Tyr	Glu	Phe	Thr	Lys	Gln	Val	Ala	Gly	Asp	Thr	Ala	Asn	20	25	30	
Val	Glu	Leu	Leu	Ile	Gly	Ala	Gly	Thr	Glu	Pro	His	Glu	Tyr	Glu	Pro	35	40	45	
Ser	Ala	Lys	Ala	Val	Ala	Lys	Ile	Gln	Asp	Ala	Asp	Thr	Phe	Val	Tyr	50	55	60	
Glu	Asn	Glu	Asn	Met	Glu	Thr	Trp	Val	Pro	Lys	Leu	Leu	Asp	Thr	Leu	65	70	75	80
Asp	Lys	Lys	Lys	Val	Lys	Thr	Ile	Lys	Ala	Thr	Gly	Asp	Met	Leu	Leu	85	90	95	
Leu	Pro	Gly	Gly	Glu	Glu	Glu	Gly	Asp	His	Asp	His	Gly	Glu	Glu		100	105	110	
Gly	His	His	His	Glu	Phe	Asp	Pro	His	Val	Trp	Leu	Ser	Pro	Val	Arg	115	120	125	
Ala	Ile	Lys	Leu	Val	Glu	His	His	Pro	Arg	His	Leu	Ser	Ala	Asp	Tyr	130	135	140	
Pro	Asp	Lys	Lys	Glu	Thr	Phe	Glu	Lys	Asn	Ala	Ala	Ala	Tyr	Ile	Glu	145	150	155	160

Lys Leu Gln Ala Leu Asp Lys Ala Tyr Ala Glu Gly Leu Ser Gln Ala
 165 170 175

Lys Gln Lys Ser Phe Val Thr Gln His Ala Ala Phe Asn Tyr Leu Ala
 180 185 190

Leu Asp Tyr Gly Thr
 195

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1003 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

TATCACAGGA TCGAACGGTA AGACAACCAC AACGACTATG ATTGGGGAAG TTTTGACTGC	60
TGCTGGCCAA CATGGTCTTT TATCAGGGAA TATCGGCTAT CCAGCTAGTC AGGTGCTCA	120
AATAGCATCA GATAAGGACA CGCTTGTTAT GGAACCTTCT TCTTTCCAAC TCATGGGTGT	180
TCAAGAATTC CATCCAGAGA TTGCGGTTAT TACCAACCTC ATGCCAACTC ATATCGACTA	240
CCATGGGTCA TTTTCGGAAT ATGTAGCAGC CAAGTGAAT ATCCAGAACA AGATGACAGC	300
AGCTGATTTT CTTGTCTTGA ACTTTAATCA AGACTTGGCA AAAGACTTGA CTTCCAAGAC	360
AGAAGCCACT GTTGTAACAT TTTCAACACT TGAAAAGGTT GATGGAGCTT ATCTGGAAGA	420
TGGTCAACTC TACTTCCGTG GTGAAGTAGT CATGGCAGCG AATGAAATCG GTGTTCCAGG	480
TAGCCACAAT GTGGAAAATG CCCTTGCGAC TATTGCTGTA GCCAAGCTTC GTGATGTGGA	540
CAATCAAACC ATCAAGGAAA CTCTTTCAGC CTTGCGGTGGT GTCAAACACC GTCTCCAGTT	600
TGTGGATGAC ATCAAGGGTG TTAAATTCTA TAACGACAGT AAATCAACTA ATATCTTGGC	660
TACTCAAAAA GCCTTGTCAG GATTGACAA CAGCAAGGTC GTCTTGATTG CAGGTGTTT	720
GGACCGTGGC AATGAGTTTG ACGAATTGGT GCCAGACATT ACTGGACTCA AGAAGATGGT	780
CATCCTGGGT CAATCTGCAG AACGTGTCAA ACGGGCAGCA GACAAGGCTG GTGTCGCTTA	840
TGTGGAGGCG ACAGATATTG CAGATGCGAC CCGCAAGGCC TATGAGCTTG CGACTCAAGG	900
AGATGTGGTT CTTCTTAGTC CTGCCAATGC TAGCTGGGAT ATGTATGCTA ACTTTGAAGT	960
ACGTGGCGAC CTCTTTATCG ACACAGTAGC GGAGTTAAAA GAA	1003

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Thr Thr Met Ile Gly
 1 5 10 15
 Glu Val Leu Thr Ala Ala Gly Gln His Gly Leu Leu Ser Gly Asn Ile
 20 25 30
 Gly Tyr Pro Ala Ser Gln Val Ala Gln Ile Ala Ser Asp Lys Asp Thr
 35 40 45
 Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met Gly Val Gln Glu Phe
 50 55 60
 His Pro Glu Ile Ala Val Ile Thr Asn Leu Met Pro Thr His Ile Asp
 65 70 75 80
 Tyr His Gly Ser Phe Ser Glu Tyr Val Ala Ala Lys Trp Asn Ile Gln
 85 90 95
 Asn Lys Met Thr Ala Ala Asp Phe Leu Val Leu Asn Phe Asn Gln Asp
 100 105 110
 Leu Ala Lys Asp Leu Thr Ser Lys Thr Glu Ala Thr Val Val Pro Phe
 115 120 125
 Ser Thr Leu Glu Lys Val Asp Gly Ala Tyr Leu Glu Asp Gly Gln Leu
 130 135 140
 Tyr Phe Arg Gly Glu Val Val Met Ala Ala Asn Glu Ile Gly Val Pro
 145 150 155 160
 Gly Ser His Asn Val Glu Asn Ala Leu Ala Thr Ile Ala Val Ala Lys
 165 170 175
 Leu Arg Asp Val Asp Asn Gln Thr Ile Lys Glu Thr Leu Ser Ala Phe
 180 185 190
 Gly Gly Val Lys His Arg Leu Gln Phe Val Asp Asp Ile Lys Gly Val
 195 200 205
 Lys Phe Tyr Asn Asp Ser Lys Ser Thr Asn Ile Leu Ala Thr Gln Lys
 210 215 220
 Ala Leu Ser Gly Phe Asp Asn Ser Lys Val Val Leu Ile Ala Gly Gly
 225 230 235 240
 Leu Asp Arg Gly Asn Glu Phe Asp Glu Leu Val Pro Asp Ile Thr Gly
 245 250 255
 Leu Lys Lys Met Val Ile Leu Gly Gln Ser Ala Glu Arg Val Lys Arg
 260 265 270
 Ala Ala Asp Lys Ala Gly Val Ala Tyr Val Glu Ala Thr Asp Ile Ala
 275 280 285
 Asp Ala Thr Arg Lys Ala Tyr Glu Leu Ala Thr Gln Gly Asp Val Val
 290 295 300
 Leu Leu Ser Pro Ala Asn Ala Ser Trp Asp Met Tyr Ala Asn Phe Glu

305	310	315	320
Val Arg Gly Asp Leu Phe Ile Asp Thr	Val Ala Glu Leu Lys Glu		
325	330	335	

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AAGTTCATCG AAGATGGTTG GGAAGTCCAC TATATCGGGG ACAAGTGTGG TATCGAACAC	60
CAAGAAATCC TTAAGTCAGG TTTGGATGTC ACCTTCCATT CTATTGCGAC TGGAAAATTG	120
CGTCGCTATT TCTCTTGCA AAATATGCTG GACGTCTTCA AAGTTGGTTG GGGGAATTGTC	180
CAATCGCTCT TTATCATGTT GCGACTGCGT CCACAGACCC TTTTTTCAAA GGGGGGCTTT	240
GTCTCAGTAC CGCTGTATTAT CGCTGCGCGT GTGTCAGGAG TGCCTGTCTT TATTCACGAA	300
TCTGACCTGT CTATGGGCTT GGCCAATAAA ATCGCCTATA AATTGCGAC TAAGATGTAT	360
TCAACCTTTG AACAAGCTTC GAGTTTGGCT AAGGTTGAGC ATGTGGGAGC GG	412

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ser Ser Ser Lys Met Val Gly Lys Ser Thr Ile Ser Gly Thr Ser Val	1	5	10	15
Val Ser Asn Thr Lys Lys Ser Leu Ser Gln Val Trp Met Ser Pro Ser	20	25	30	
Ile Leu Leu Arg Leu Glu Asn Cys Val Ala Ile Ser Leu Gly Lys Ile	35	40	45	
Cys Trp Thr Ser Ser Lys Leu Val Gly Glu Leu Ser Asn Arg Ser Leu	50	55	60	
Ser Cys Cys Asp Cys Val His Arg Pro Phe Phe Gln Arg Gly Ala Leu	65	70	75	80
Ser Gln Tyr Arg Leu Ser Leu Arg Val Cys Gln Glu Cys Leu Ser	85	90	95	
Leu Phe Thr Asn Leu Thr Cys Leu Trp Ala Trp Pro Ile Lys Ser Pro				

50		55		60
Val Pro Glu Ile Asp	Pro Ser Gln Ile Asp	Ser Arg Val Gln Ile Glu		
65	70	75	80	
Asn Val Met Val Ser	Asp Lys Glu Val Ser	Ile Thr Ser Asp Gln Glu		
	85	90	95	
Thr Leu Asp Arg Ile	Asp Lys Ile Ile Ala Val	Leu Pro Thr Ser Glu		
	100	105	110	
Arg Ile Thr Gly Asn Tyr	Ser Gly Ser Val Pro	Leu Gln Ala Ile Asp		
	115	120	125	
Arg Asn Gly Val Val	Leu Pro Ala Val Ile	Thr Pro Phe Asp Thr Ile		
	130	135	140	
Met Lys Val Thr Thr	Lys Pro Val Ala Pro	Ser Ser Ser Thr Ser Asn		
	145	150	155	160
Ser Ser Thr Ser Ser	Ser Ser Glu Thr Ser	Ser Ser Thr Lys Ala Thr		
	165	170	175	
Ser Ser Lys Thr Asn				
	180			

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GCACCAGATG GGGCACAAGG TTCAGGGATC AGATGTTGAA AAGTACTACT TTACCCAACG	60
CGGTCTTGAG CAGGCAGGAA TTACCATTCT TCCTTTTGAT GAAAAAATC TAGACGGTGA	120
TATGGAAATT ATCGCTGGAA ATGCCTTTTCG TCCAGATAAC AACGTCGAAA TTGCCTATGC	180
GGACCAAAAT GGTATCAGCT ACAAACGTTA CCATGAGTTT CTAGGTAGCT TTATGCGTGA	240
CTTTGTTAGC ATGGGAGTAG CAGGAGCACA TGGAAAACT TCAACGACAG GTATGTTGTC	300
TCATGTCTTG TCTCACATTA CAGATACCAG CTTCTTGATT GGAGATGGGA CAGGTCGTGG	360
TTCGGCCAAT GCCAAATATT TTGTCTTTGA ATCTGACGAA TATGAGCGTC ACTTCATGCC	420
TTACCACCCA GAATACTCTA TTATCACCAA CATTGACTTT GACCATCCAG ATTATTTTAC	480
AAGTCTCGAG GATGTTTTTA ATGCCTTTAA CGACTATGCC AAACAAATCA CCAAGGGTCT	540
TTTTGTCTAT GGTGAAGATG CTGAATTGCG TAAGATTACG TCTGATGCAC CAATTTATTA	600
TTATGGTTTT GAAGCTGAAG GCAATGACTT TGTAAGTAGT GATCTTCTTC GTTCAATAAC	660
TGGTTCAACC TTCACCGTTC ATTTCCGTGG ACAAACCTTG GGGCAATTCC ACATTCCAAC	720
CTTTGGTCGT CACAATATCA TGAATGCGAC AGCCGTTATT GGTCTTCTTT ACACAGCAGG	780

ATTTGATTTG AACTTGGTGC GTGAGCACTT GAAAACATTT GCCGGTGTTA AACGTCGTTT 840
 CACTGAGAAA ATTGTCAATG ATACAGTGAT TATCGATGAC TTTGCCCACC ATCCAACAGA 900
 AATTATTGCG ACCTTGGATG CGGCTCGTCA GAAATACCCA AGCAAGGAAA TTGTAGCAGT 960
 CTTTCAACCG CATACTTTA CAAGAACCAT TGCCTTGTTG GACGACTTTG CCCATGCTTT 1020
 AAACCAAGCA GATGCTGTTT ATCTAGCGCA AATTTATGGC TCGGCTCGTG AAGTAGATCA 1080
 TGGTGACGTT AAGGTAGAAG ACCTAGCCAA CAAAATCAAC AAAAAACACC AAGTGATTAC 1140
 TGTTGAAAAT GTTTCTCCAC TCCTAGACCA TGACAATGCT GTTTACGTCT TTATGGGAGC 1200
 AGGAGACATC CAAACCTATG AATACTCATT TGAGCGTCTC TTGTCTAACT TGACAAGCAA 1260
 TGTTCAA 1267

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 422 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

His	Gln	Met	Gly	His	Lys	Val	Gln	Gly	Ser	Asp	Val	Glu	Lys	Tyr	Tyr	1	5	10	15
Phe	Thr	Gln	Arg	Gly	Leu	Glu	Gln	Ala	Gly	Ile	Thr	Ile	Leu	Pro	Phe	20	25	30	
Asp	Glu	Lys	Asn	Leu	Asp	Gly	Asp	Met	Glu	Ile	Ile	Ala	Gly	Asn	Ala	35	40	45	
Phe	Arg	Pro	Asp	Asn	Asn	Val	Glu	Ile	Ala	Tyr	Ala	Asp	Gln	Asn	Gly	50	55	60	
Ile	Ser	Tyr	Lys	Arg	Tyr	His	Glu	Phe	Leu	Gly	Ser	Phe	Met	Arg	Asp	65	70	75	80
Phe	Val	Ser	Met	Gly	Val	Ala	Gly	Ala	His	Gly	Lys	Thr	Ser	Thr	Thr	85	90	95	
Gly	Met	Leu	Ser	His	Val	Leu	Ser	His	Ile	Thr	Asp	Thr	Ser	Phe	Leu	100	105	110	
Ile	Gly	Asp	Gly	Thr	Gly	Arg	Gly	Ser	Ala	Asn	Ala	Lys	Tyr	Phe	Val	115	120	125	
Phe	Glu	Ser	Asp	Glu	Tyr	Glu	Arg	His	Phe	Met	Pro	Tyr	His	Pro	Glu	130	135	140	
Tyr	Ser	Ile	Ile	Thr	Asn	Ile	Asp	Phe	Asp	His	Pro	Asp	Tyr	Phe	Thr	145	150	155	160
Ser	Leu	Glu	Asp	Val	Phe	Asn	Ala	Phe	Asn	Asp	Tyr	Ala	Lys	Gln	Ile				

228

	165		170		175
Thr Lys Gly Leu Phe Val Tyr Gly Glu Asp Ala Glu Leu Arg Lys Ile	180		185		190
Thr Ser Asp Ala Pro Ile Tyr Tyr Tyr Gly Phe Glu Ala Glu Gly Asn	195		200		205
Asp Phe Val Ala Ser Asp Leu Leu Arg Ser Ile Thr Gly Ser Thr Phe	210		215		220
Thr Val His Phe Arg Gly Gln Asn Leu Gly Gln Phe His Ile Pro Thr	225		230		235
Phe Gly Arg His Asn Ile Met Asn Ala Thr Ala Val Ile Gly Leu Leu	245		250		255
Tyr Thr Ala Gly Phe Asp Leu Asn Leu Val Arg Glu His Leu Lys Thr	260		265		270
Phe Ala Gly Val Lys Arg Arg Phe Thr Glu Lys Ile Val Asn Asp Thr	275		280		285
Val Ile Ile Asp Asp Phe Ala His His Pro Thr Glu Ile Ile Ala Thr	290		295		300
Leu Asp Ala Ala Arg Gln Lys Tyr Pro Ser Lys Glu Ile Val Ala Val	305		310		315
Phe Gln Pro His Thr Phe Thr Arg Thr Ile Ala Leu Leu Asp Asp Phe	325		330		335
Ala His Ala Leu Asn Gln Ala Asp Ala Val Tyr Leu Ala Gln Ile Tyr	340		345		350
Gly Ser Ala Arg Glu Val Asp His Gly Asp Val Lys Val Glu Asp Leu	355		360		365
Ala Asn Lys Ile Asn Lys Lys His Gln Val Ile Thr Val Glu Asn Val	370		375		380
Ser Pro Leu Leu Asp His Asp Asn Ala Val Tyr Val Phe Met Gly Ala	385		390		395
Gly Asp Ile Gln Thr Tyr Glu Tyr Ser Phe Glu Arg Leu Leu Ser Asn	405		410		415
Leu Thr Ser Asn Val Gln	420				

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

TTTAAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT

GGTTTCTAAA	AGGGAAAATG	GAAAGAAAACG	ACTTGTTTCAT	TTTCTGCTGT	TGACTAGCAT	120
GGGAGTTCAA	TTGTTGCCGG	CCAGTGCTTT	TGGGTTGACC	AGCCAGATTT	TATCTGCCTA	180
TAATAGTCAG	CTTTCTATCG	GAGTCGGGGA	ACATTTACCA	GAGCCTCTGA	AAATCGAAGG	240
TTATCAATAT	ATTGGTTATA	TCAAAACTAA	GAAACAGGAT	AATACAGAGC	TTTCAAGGAC	300
AGTTGATGGG	AAATACTCTG	CTCAAAGAGA	TAGTCAACCA	AACTCTACAA	AAACATCAGA	360
TGTAGTTCAT	TCAGCTGATT	TAGAATGGAA	CCAAGGACAG	GGGAAGGTTA	GTTTACAAGG	420
TGAAGCATCA	GGGGATGATG	GACTTTCAGA	AAAATCTTCT	ATAGCAGCAG	ACAATCTATC	480
TTCTAATGAT	TCATTGCGAA	GTCAAGTTGA	GCAGAATCCG	GATCACAAAG	GAGAATCTGT	540
AGTTGACCA	ACAGTGCCAG	AACAAGGAAA	TCCTGTGTCT	GCTACAACGG	TGCAGAGTGC	600
GGAAGAGGAA	GTATTGGCGA	CGACAAATGA	TCGACCAGAG	TATAAACTTC	CATTGGAAAC	660
CAAAGGCACG	CAAGAACCCG	GTCATGAGGG	TGAAGCCGCA	GTCCGTGAAG	ACTTACCAGT	720
CTACACTAAG	CCACTAGAAA	CCAAAGGTAC	ACAAGGACCC	GGACATGAAG	GTGAAGCTGC	780
AGTTGCGGAG	GAAGAACCAG	CTTACACAGA	ACCGTTAGCA	ACGAAAGGCA	CGCAAGAGCC	840
AGGTCATGAG	GGCAAAGCTA	CAGTCCGCGA	AGAGACTCTA	GAGTACACGG	AACCGGTAGC	900
GACAAAAGGC	ACACAAGAAC	CCGAACATGA	GGGCGAaCGG	sCAGTAGAAG	AAGAACTTCC	960
GGCTTTAGAG	GTCACTACAC	GAAATAGAAC	GGAAATCCAG	AATATTCCTT	ATACAACAGA	1020
AGAAATTCAG	GATCCAACAC	TTCTGAAAAA	TCGTGCTAAG	ATTGAACGAC	AAGGGCAAGC	1080
AGGGACACGT	ACAATTCAAT	ATGAAGACTA	CATCGTAAAT	GGTAATGTCG	TAGAAACTAA	1140
AGAAGTGTC	CGAACTGAAG	TAGCTCCGGT	CAACGAAGTC	GTTAAAGTAG	GAACACTTGT	1200
GAAAGTTAAA	CCTACAGTAG	AAATTACAAA	CTTAACAAAA	GTTGAGAACA	AAAAATCTAT	1260
AACTGTAAGT	TATAACTTAA	TAGACACTAC	CTCAGCATAT	GTTTCTGCAA	AAACGCAAGT	1320
TTTCCATGGA	GACAAGCTAG	TTAAAGAGGT	GGATATAGAA	AATCCTGCCA	AAGAGCAAGT	1380
AATATCAGGT	TTAGATTACT	ACACACCGTA	TACAGTTAAA	ACACACCTAA	CTTATAATTT	1440
GGGTGAAAAT	AATGAGGAAA	ATACTGAAAC	ATCAACTCAA	GATTTCCAAT	TAGAGTATAA	1500
GAAATAGAG	ATTAAAGATA	TTGATTCAAGT	AGAATTATAC	GGTAAAGAAA	ATGATCGTTA	1560
TCGTAGATAT	TTAAGTCTAA	GTGAAGCGCC	GACTGATACG	GCTAAATACT	TTGTAAAGT	1620
GAAATCAGAT	CGCTTCAAAG	AAATGTACCT	ACCTGTAAAA	TCTATTACAG	AAAATACGGA	1680
TGGAACGTAT	AAAGTGACGG	TAGCCGTTGA	TCAACTTGTC	GAAGAAGGTA	CAGACGGTTA	1740
CAAAGATGAT	TACACATTTA	CTGTAGCTAA	ATCTAAAGCA	GAGCAACCAG	GAGTTTACAC	1800
ATCCTTTAAA	CAGCTGGTAA	CAGCCATGCA	AAGCAATCTG	TCTGGTGTCT	ATACATTGGC	1860
TTCAGATATG	ACCGCAGATG	AGGTGAGCTT	AGGCGATAAG	CAGACAAGTT	ATCTCACAGG	1920

TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT 1980
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAAC 2040
 TGTTTCTGCT GATAGTAAAG AAAATGTGCG AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 2100
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 2160
 AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 2220
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 2280
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 2340
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 2400
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 2460
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 2520
 TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 2580
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 2640
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 2700
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 2760
 CAACATAGAA AACTGATGC CATTCTACAA TAAAGACCTA GTAGTTCACT ATGGTAACAA 2820
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTGA GATGTTGTGC CGATGAAAGA 2880
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 2940
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TATATAACAG 3000
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 3060
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 3120
 C 3121

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1040 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
 1 5 10 15
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
 20 25 30
 His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser
 35 40 45

Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
 50 55 60
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
 65 70 75 80
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
 85 90 95
 Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
 100 105 110
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
 115 120 125
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
 130 135 140
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
 145 150 155 160
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
 165 170 175
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
 180 185 190
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
 195 200 205
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
 210 215 220
 Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
 225 230 235 240
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
 245 250 255
 Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu
 260 265 270
 Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val
 275 280 285
 Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr
 290 295 300
 Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro
 305 310 315 320
 Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro
 325 330 335
 Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg
 340 345 350
 Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu
 355 360 365
 Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg
 370 375 380

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val
 385 390 395 400
 Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn
 405 410 415
 Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala
 420 425 430
 Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys
 435 440 445
 Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu
 450 455 460
 Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu
 465 470 475 480
 Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln
 485 490 495
 Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu
 500 505 510
 Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg Tyr Leu Ser Leu Ser Glu
 515 520 525
 Ala Pro Thr Asp Thr Ala Lys Tyr Phe Val Lys Val Lys Ser Asp Arg
 530 535 540
 Phe Lys Glu Met Tyr Leu Pro Val Lys Ser Ile Thr Glu Asn Thr Asp
 545 550 555 560
 Gly Thr Tyr Lys Val Thr Val Ala Val Asp Gln Leu Val Glu Glu Gly
 565 570 575
 Thr Asp Gly Tyr Lys Asp Asp Tyr Thr Phe Thr Val Ala Lys Ser Lys
 580 585 590
 Ala Glu Gln Pro Gly Val Tyr Thr Ser Phe Lys Gln Leu Val Thr Ala
 595 600 605
 Met Gln Ser Asn Leu Ser Gly Val Tyr Thr Leu Ala Ser Asp Met Thr
 610 615 620
 Ala Asp Glu Val Ser Leu Gly Asp Lys Gln Thr Ser Tyr Leu Thr Gly
 625 630 635 640
 Ala Phe Thr Gly Ser Leu Ile Gly Ser Asp Gly Thr Lys Ser Tyr Ala
 645 650 655
 Ile Tyr Asp Leu Lys Lys Pro Leu Phe Asp Thr Leu Asn Gly Ala Thr
 660 665 670
 Val Arg Asp Leu Asp Ile Lys Thr Val Ser Ala Asp Ser Lys Glu Asn
 675 680 685
 Val Ala Ala Leu Ala Lys Ala Ala Asn Ser Ala Asn Ile Asn Asn Val
 690 695 700
 Ala Val Glu Gly Lys Ile Ser Gly Ala Lys Ser Val Ala Gly Leu Val
 705 710 715 720

Ala	Ser	Ala	Thr	Asn	Thr	Val	Ile	Glu	Asn	Ser	Ser	Phe	Thr	Gly	Lys		
				725					730					735			
Leu	Ile	Ala	Asn	His	Gln	Asp	Ser	Asn	Lys	Asn	Asp	Thr	Gly	Gly	Ile		
			740					745					750				
Val	Gly	Asn	Ile	Thr	Gly	Asn	Ser	Ser	Arg	Val	Asn	Lys	Val	Arg	Val		
		755					760					765					
Asp	Ala	Leu	Ile	Ser	Thr	Asn	Ala	Arg	Asn	Asn	Asn	Gln	Thr	Ala	Gly		
	770					775					780						
Gly	Ile	Val	Gly	Arg	Leu	Glu	Asn	Gly	Ala	Leu	Ile	Ser	Asn	Ser	Val		
785					790					795					800		
Ala	Thr	Gly	Glu	Ile	Arg	Asn	Gly	Gln	Gly	Tyr	Ser	Arg	Val	Gly	Gly		
				805					810					815			
Ile	Val	Gly	Ser	Thr	Trp	Gln	Asn	Gly	Arg	Val	Asn	Asn	Val	Val	Ser		
			820					825					830				
Asn	Val	Asp	Val	Gly	Asp	Gly	Tyr	Val	Ile	Thr	Gly	Asp	Gln	Tyr	Ala		
		835					840					845					
Ala	Ala	Asp	Val	Lys	Asn	Ala	Ser	Thr	Ser	Val	Asp	Asn	Arg	Lys	Ala		
	850					855					860						
Asp	Arg	Phe	Ala	Thr	Lys	Leu	Ser	Lys	Asp	Gln	Ile	Asp	Ala	Lys	Val		
865					870					875					880		
Ala	Asp	Tyr	Gly	Ile	Thr	Val	Thr	Leu	Asp	Asp	Thr	Gly	Gln	Asp	Leu		
				885				890						895			
Lys	Arg	Asn	Leu	Arg	Glu	Val	Asp	Tyr	Thr	Arg	Leu	Asn	Lys	Ala	Glu		
			900					905					910				
Ala	Glu	Arg	Lys	Val	Ala	Tyr	Ser	Asn	Ile	Glu	Lys	Leu	Met	Pro	Phe		
		915					920					925					
Tyr	Asn	Lys	Asp	Leu	Val	Val	His	Tyr	Gly	Asn	Lys	Val	Ala	Thr	Thr		
	930					935					940						
Asp	Lys	Leu	Tyr	Thr	Thr	Glu	Leu	Leu	Asp	Val	Val	Pro	Met	Lys	Asp		
945					950					955					960		
Asp	Glu	Val	Val	Thr	Asp	Ile	Asn	Asn	Lys	Lys	Asn	Ser	Ile	Asn	Lys		
				965					970					975			
Val	Met	Leu	His	Phe	Lys	Asp	Asn	Thr	Val	Glu	Tyr	Leu	Asp	Val	Thr		
			980					985					990				
Phe	Lys	Glu	Asn	Phe	Ile	Asn	Ser	Gln	Val	Ile	Glu	Tyr	Asn	Val	Thr		
		995					1000					1005					
Gly	Lys	Glu	Tyr	Ile	Phe	Thr	Pro	Glu	Ala	Phe	Val	Ser	Asp	Tyr	Thr		
	1010					1015					1020						
Ala	Ile	Thr	Asn	Asn	Val	Leu	Ser	Asp	Leu	Gln	Asn	Val	Thr	Leu	Asn		
	1025					1030				1035					1040		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TTTTAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT	60
GGTTTCTAAA AGGAAAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGACTIONCAT	120
GGGAGTTCAA TTGTTGCCGG CCAGTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA	180
TAATAGTCAG CTTTCTATCG GAGTCGGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG	240
TTATCAATAT ATTGGTTATA TCAAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC	300
AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA	360
TGTAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGAAGGTTA GTTTACAAGG	420
TGAAGCATCA GGGGATGATG GACTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC	480
TTCTAATGAT TCATTCGCAA GTCAAGTTGA GCAGAAATCCG GATCACAAAG GAGAATCTGT	540
AGTTCGACCA ACAGTGCCAG AACAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC	600
GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTGGAAAC	660
CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT	720
CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC	780
AGTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC	840
AGGTCATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACCGGTAGC	900
GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAACTTCC	960
GGCTTTAGAG GTCACTACAC GAAATAGAAC GGAAATCCAG AATATTCCTT ATACAACAGA	1020
AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC	1080
AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCTG TAGAACTAA	1140
AGAAGTGTCA CGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT	1200
GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT	1260
AACTGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTTCTGCAA AAACGCAAGT	1320
TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT	1380
AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT	1440
GGGTGAAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTCCAAT TAGAGTATAA	1500
GAAAATAGAG ATTAAAGATA TTGATTCAGT AGAATTATAC GGTAAAGAAA ATGATCGTTA	1560
TCGTAGA	1567

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 522 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

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Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
1          5          10          15
Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
20        25        30
His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser
35        40        45
Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
50        55        60
Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
65        70        75        80
Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
85        90        95
Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
100       105       110
Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
115       120       125
Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
130       135       140
Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
145       150       155       160
Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
165       170       175
Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
180       185       190
Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
195       200       205
Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
210       215       220
Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
225       230       235       240
Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
245       250       255
Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu

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236

260 265 270

Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val
275 280 285

Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr
290 295 300

Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro
305 310 315 320

Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro
325 330 335

Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg
340 345 350

Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu
355 360 365

Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg
370 375 380

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val
385 390 395 400

Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn
405 410 415

Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala
420 425 430

Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys
435 440 445

Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu
450 455 460

Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu
465 470 475 480

Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln
485 490 495

Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu
500 505 510

Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg
515 520

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT

GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA	120
TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA	180
CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC	240
ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC	300
TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG	360
TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT	420
GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAC	480
TGTTTCTGCT GATAGTAAAG AAAATGTGCG AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA	540
TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT	600
AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA	660
TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG	720
TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA	780
CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT	840
TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC	900
TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA	960
TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA	1020
TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT	1080
TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT	1140
AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG	1200
CAACATAGAA AACTGATGC CATTCTACAA TAAAGACCTA GTAGTTCACT ATGGTAACAA	1260
AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAAGA	1320
TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA	1380
TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAACT TCATAAACAG	1440
TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT	1500
TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA	1560
C	1561

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Arg	Arg	Tyr	Leu	Ser	Leu	Ser	Glu	Ala	Pro	Thr	Asp	Thr	Ala	Lys	Tyr	1	5	10	15
Phe	Val	Lys	Val	Lys	Ser	Asp	Arg	Phe	Lys	Glu	Met	Tyr	Leu	Pro	Val	20	25	30	
Lys	Ser	Ile	Thr	Glu	Asn	Thr	Asp	Gly	Thr	Tyr	Lys	Val	Thr	Val	Ala	35	40	45	
Val	Asp	Gln	Leu	Val	Glu	Glu	Gly	Thr	Asp	Gly	Tyr	Lys	Asp	Asp	Tyr	50	55	60	
Thr	Phe	Thr	Val	Ala	Lys	Ser	Lys	Ala	Glu	Gln	Pro	Gly	Val	Tyr	Thr	65	70	75	80
Ser	Phe	Lys	Gln	Leu	Val	Thr	Ala	Met	Gln	Ser	Asn	Leu	Ser	Gly	Val	85	90	95	
Tyr	Thr	Leu	Ala	Ser	Asp	Met	Thr	Ala	Asp	Glu	Val	Ser	Leu	Gly	Asp	100	105	110	
Lys	Gln	Thr	Ser	Tyr	Leu	Thr	Gly	Ala	Phe	Thr	Gly	Ser	Leu	Ile	Gly	115	120	125	
Ser	Asp	Gly	Thr	Lys	Ser	Tyr	Ala	Ile	Tyr	Asp	Leu	Lys	Lys	Pro	Leu	130	135	140	
Phe	Asp	Thr	Leu	Asn	Gly	Ala	Thr	Val	Arg	Asp	Leu	Asp	Ile	Lys	Thr	145	150	155	160
Val	Ser	Ala	Asp	Ser	Lys	Glu	Asn	Val	Ala	Ala	Leu	Ala	Lys	Ala	Ala	165	170	175	
Asn	Ser	Ala	Asn	Ile	Asn	Asn	Val	Ala	Val	Glu	Gly	Lys	Ile	Ser	Gly	180	185	190	
Ala	Lys	Ser	Val	Ala	Gly	Leu	Val	Ala	Ser	Ala	Thr	Asn	Thr	Val	Ile	195	200	205	
Glu	Asn	Ser	Ser	Phe	Thr	Gly	Lys	Leu	Ile	Ala	Asn	His	Gln	Asp	Ser	210	215	220	
Asn	Lys	Asn	Asp	Thr	Gly	Gly	Ile	Val	Gly	Asn	Ile	Thr	Gly	Asn	Ser	225	230	235	240
Ser	Arg	Val	Asn	Lys	Val	Arg	Val	Asp	Ala	Leu	Ile	Ser	Thr	Asn	Ala	245	250	255	
Arg	Asn	Asn	Asn	Gln	Thr	Ala	Gly	Gly	Ile	Val	Gly	Arg	Leu	Glu	Asn	260	265	270	
Gly	Ala	Leu	Ile	Ser	Asn	Ser	Val	Ala	Thr	Gly	Glu	Ile	Arg	Asn	Gly	275	280	285	
Gln	Gly	Tyr	Ser	Arg	Val	Gly	Gly	Ile	Val	Gly	Ser	Thr	Trp	Gln	Asn	290	295	300	
Gly	Arg	Val	Asn	Asn	Val	Val	Ser	Asn	Val	Asp	Val	Gly	Asp	Gly	Tyr	305	310	315	320

2025-12-26 14:23:20

Val Ile Thr Gly Asp Gln Tyr Ala Ala Ala Asp Val Lys Asn Ala Ser
 325 330 335
 Thr Ser Val Asp Asn Arg Lys Ala Asp Arg Phe Ala Thr Lys Leu Ser
 340 345 350
 Lys Asp Gln Ile Asp Ala Lys Val Ala Asp Tyr Gly Ile Thr Val Thr
 355 360 365
 Leu Asp Asp Thr Gly Gln Asp Leu Lys Arg Asn Leu Arg Glu Val Asp
 370 375 380
 Tyr Thr Arg Leu Asn Lys Ala Glu Ala Glu Arg Lys Val Ala Tyr Ser
 385 390 395 400
 Asn Ile Glu Lys Leu Met Pro Phe Tyr Asn Lys Asp Leu Val Val His
 405 410 415
 Tyr Gly Asn Lys Val Ala Thr Thr Asp Lys Leu Tyr Thr Thr Glu Leu
 420 425 430
 Leu Asp Val Val Pro Met Lys Asp Asp Glu Val Val Thr Asp Ile Asn
 435 440 445
 Asn Lys Lys Asn Ser Ile Asn Lys Val Met Leu His Phe Lys Asp Asn
 450 455 460
 Thr Val Glu Tyr Leu Asp Val Thr Phe Lys Glu Asn Phe Ile Asn Ser
 465 470 475 480
 Gln Val Ile Glu Tyr Asn Val Thr Gly Lys Glu Tyr Ile Phe Thr Pro
 485 490 495
 Glu Ala Phe Val Ser Asp Tyr Thr Ala Ile Thr Asn Asn Val Leu Ser
 500 505 510
 Asp Leu Gln Asn Val Thr Leu Asn
 515 520

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTTTGGTTTT GAAGGAAGTA AGCGTGGACA ATTTGCTGTA GAAGGAATCA ATCAACTTCG	60
TGAGCATGTA GACACTCTAT TGATTATCTC AAACAACAAT TTGCTTGAAA TTGTTGATAA	120
GAAACACCG CTTTTGGAGG CTCTTAGCGA AGCGGATAAC GTTCTTCGTC AAGGTGTTCA	180
AGGGATTACC GATTTGATTA CCAATCCAGG ATTGATTAAC CTTGACTTTG CCGATGTGAA	240
AACGGTAATG GCAAACAAAG GGAATGCTCT TATGGGTATT GGTATCGGTA GTGGAGAAGA	300
ACGTGTGGTA GAAGCGGCAC GTAAGGCAAT CTATTCACCA CTTCTTGAAA CAACTATTGA	360

CGGTGCTGAG GATGTTATCG TCAACGTTAC TGGTGGTCTT GACTTAACCT TGATTGAGGC 420
 AGAAGAGGCT TCACAAATTG TGAACCAGGC AGCAGGTCAA GGAGTGAACA TCTGGCTCGG 480
 TACTTCAATT GATGAAAGTA TGCCTGATGA AATTCGTGTA ACAGTTGTTG CAACGGGTGT 540
 TCGTCAAGAC CGCGTAGAAA AGGTTGTGGC TCCACAAGCT AGATCTGCTA CTAACCTACCG 600
 TGAGACAGTG AAACCAGCTC ATTCACATGG CTTTGATCGT CATTTTGATA TGGCAGAAAC 660
 AGTTGAATTG CCAAAACAAA ATCCACGTCG TTTGGAACCA ACTCAGGCAT CTGCTTTTGG 720
 TGATTGGGAT CTTCCGCGTG AATCGATTGT TCGTACAACA GATTCAGTCG TTTCTCCAGT 780
 CGAGCGCTTT GAAGCCCCAA TTTCACAAGA TGAAGATGAA TTGGATACAC CTCCATTTTT 840
 CAAAAATCGT 850

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Phe	Gly	Phe	Glu	Gly	Ser	Lys	Arg	Gly	Gln	Phe	Ala	Val	Glu	Gly	Ile	1	5	10	15
Asn	Gln	Leu	Arg	Glu	His	Val	Asp	Thr	Leu	Leu	Ile	Ile	Ser	Asn	Asn	20	25	30	
Asn	Leu	Leu	Glu	Ile	Val	Asp	Lys	Lys	Thr	Pro	Leu	Leu	Glu	Ala	Leu	35	40	45	
Ser	Glu	Ala	Asp	Asn	Val	Leu	Arg	Gln	Gly	Val	Gln	Gly	Ile	Thr	Asp	50	55	60	
Leu	Ile	Thr	Asn	Pro	Gly	Leu	Ile	Asn	Leu	Asp	Phe	Ala	Asp	Val	Lys	65	70	75	80
Thr	Val	Met	Ala	Asn	Lys	Gly	Asn	Ala	Leu	Met	Gly	Ile	Gly	Ile	Gly	85	90	95	
Ser	Gly	Glu	Glu	Arg	Val	Val	Glu	Ala	Ala	Arg	Lys	Ala	Ile	Tyr	Ser	100	105	110	
Pro	Leu	Leu	Glu	Thr	Thr	Ile	Asp	Gly	Ala	Glu	Asp	Val	Ile	Val	Asn	115	120	125	
Val	Thr	Gly	Gly	Leu	Asp	Leu	Thr	Leu	Ile	Glu	Ala	Glu	Glu	Ala	Ser	130	135	140	
Gln	Ile	Val	Asn	Gln	Ala	Ala	Gly	Gln	Gly	Val	Asn	Ile	Trp	Leu	Gly	145	150	155	160
Thr	Ser	Ile	Asp	Glu	Ser	Met	Arg	Asp	Glu	Ile	Arg	Val	Thr	Val	Val	165	170	175	

Ala Thr Gly Val Arg Gln Asp Arg Val Glu Lys Val Val Ala Pro Gln
 180 185 190

Ala Arg Ser Ala Thr Asn Tyr Arg Glu Thr Val Lys Pro Ala His Ser
 195 200 205

His Gly Phe Asp Arg His Phe Asp Met Ala Glu Thr Val Glu Leu Pro
 210 215 220

Lys Gln Asn Pro Arg Arg Leu Glu Pro Thr Gln Ala Ser Ala Phe Gly
 225 230 235 240

Asp Trp Asp Leu Arg Arg Glu Ser Ile Val Arg Thr Thr Asp Ser Val
 245 250 255

Val Ser Pro Val Glu Arg Phe Glu Ala Pro Ile Ser Gln Asp Glu Asp
 260 265 270

Glu Leu Asp Thr Pro Pro Phe Phe Lys Asn Arg
 275 280

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CTACTACCTC TCGAGAGAAA GTGACCTAGA GGTGACCGTT TTTGACCATG AGCAAGGTCA	60
AGCCACCAAG GCCGCAGCAG GAATTATCAG TCCTTGTTT TCCAAACGCC GTAATAAAGC	120
CTGGTACAAG ATGGCGCGCT TGGGGGCTGA TTTTATGTG GATTTATTAG CTGATTTAGA	180
GAAATCAGGA CAAGAAATCG ACTTTTACCA GCGTTCGGGA GTCTTTCTCT TGAAAAAGGA	240
TGAATCCAAT TTGAAGAAC TTTATCAACT GGCCCTCCAG CGCAGAGAAG AATCTCCCTT	300
GATAGGGCAA TTAGCCATTC TGAACCAAGC CTCAGCTAAT GAATTATTCC CTGGTTTGCA	360
GGGATTTGAC CGCCTGCTCT ATGCTTCTGG TGGAGCGAGA GTAGATGGCC AACTTTTAGT	420
GACTCGTTTG CTGGAAGTCA GTCATGTCAA GCTGGTCAAA GAAAAAGTGA CTCTGACACC	480
GTTAGCATCA GGCTACCAGA TTGGTGAAGA GGAGTTTGAG CAGGTTATTT TGGCGACGGG	540
AGCTTGTTG GGGGACATGT TAGAGCCTTT AGGTTATGAA GTGGATGTCC GTCCTCAAAA	600
AGGACAAC TA CGAGATTATC AGCTTGCCCA AGACATGGAA GATTACCCTG TTGTCATGCC	660
AGAAGGGGAG TGGGATTGA TTCCCTTTC AGGTGGGAAA TTATCCTTAG GCGCTACCCA	720
CGAAAATGAC ATGGGATTTG ATTTGACGGT AGATGAAACC TTGCTCCAAC AAATGGAGGA	780
GGCCACCTTG ACTCACTATC TGATTTTGGC TGAAGCTACT TCAAAATCTG AGCGTGTGG	840
AATCCGTGCC TACACCAGTG ATTTCTCTCC TTTCTTTGGG CAGGTGCCTG ACTTAACTGG	900

TGTCTATGCA GCCAGTGGAC TAGGTTTCATC AGGCCTCACA ACTGGTCCTA TCATTGGTTA 960
 CCATCTAGCC CAACTGATCC AAGACAAGGA GTTGACCTTG GACCCCTCTAA ATTACCCAAT 1020
 TGAAAACTAT GTCAAACGAG TAAAAAGCGA A 1051

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Tyr	Tyr	Leu	Ser	Arg	Glu	Ser	Asp	Leu	Glu	Val	Thr	Val	Phe	Asp	His	1	5	10	15
Glu	Gln	Gly	Gln	Ala	Thr	Lys	Ala	Ala	Ala	Gly	Ile	Ile	Ser	Pro	Trp	20	25	30	
Phe	Ser	Lys	Arg	Arg	Asn	Lys	Ala	Trp	Tyr	Lys	Met	Ala	Arg	Leu	Gly	35	40	45	
Ala	Asp	Phe	Tyr	Val	Asp	Leu	Leu	Ala	Asp	Leu	Glu	Lys	Ser	Gly	Gln	50	55	60	
Glu	Ile	Asp	Phe	Tyr	Gln	Arg	Ser	Gly	Val	Phe	Leu	Leu	Lys	Lys	Asp	65	70	75	80
Glu	Ser	Asn	Leu	Glu	Glu	Leu	Tyr	Gln	Leu	Ala	Leu	Gln	Arg	Arg	Glu	85	90	95	
Glu	Ser	Pro	Leu	Ile	Gly	Gln	Leu	Ala	Ile	Leu	Asn	Gln	Ala	Ser	Ala	100	105	110	
Asn	Glu	Leu	Phe	Pro	Gly	Leu	Gln	Gly	Phe	Asp	Arg	Leu	Leu	Tyr	Ala	115	120	125	
Ser	Gly	Gly	Ala	Arg	Val	Asp	Gly	Gln	Leu	Leu	Val	Thr	Arg	Leu	Leu	130	135	140	
Glu	Val	Ser	His	Val	Lys	Leu	Val	Lys	Glu	Lys	Val	Thr	Leu	Thr	Pro	145	150	155	160
Leu	Ala	Ser	Gly	Tyr	Gln	Ile	Gly	Glu	Glu	Glu	Phe	Glu	Gln	Val	Ile	165	170	175	
Leu	Ala	Thr	Gly	Ala	Trp	Leu	Gly	Asp	Met	Leu	Glu	Pro	Leu	Gly	Tyr	180	185	190	
Glu	Val	Asp	Val	Arg	Pro	Gln	Lys	Gly	Gln	Leu	Arg	Asp	Tyr	Gln	Leu	195	200	205	
Ala	Gln	Asp	Met	Glu	Asp	Tyr	Pro	Val	Val	Met	Pro	Glu	Gly	Glu	Trp	210	215	220	
Asp	Leu	Ile	Pro	Phe	Ala	Gly	Gly	Lys	Leu	Ser	Leu	Gly	Ala	Thr	His				

(2) INFORMATION FOR SEQ ID NO: 127:

(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TAAGGTCAAA	AGTCAGACCG	CTAAGAAAGT	GCTAGAAAAG	ATTGGAGCTG	ACTCGGTTAT	60
CTCGCCAGAG	TATGAAATGG	GGCAGTCTCT	AGCACAGACC	ATTCTTTTCC	ATAATAGTGT	120
TGATGTCTTT	CAGTTGGATA	AAAATGTGTC	TATCGTGGAG	ATGAAAATTC	CTCAGTCTTG	180
GGCAGGTCAA	AGTCTGAGTA	AATTAGACCT	CCGTGGCAAA	TACAATCTGA	ATATTTTGGG	240
TTTCCGAGAG	CAGGAAAATT	CCCCATTGGA	TGTTGAATTT	GGACCAGATG	ACCTCTTGAA	300
AGCAGATACC	TATATTTTGG	CAGTCATCAA	CAACCAGTAT	TTGGATACCC	TA	352

(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Val Lys Ser Gln Thr Ala Lys Lys Val Leu Glu Lys Ile Gly Ala
1 5 10 15

Asp Ser Val Ile Ser Pro Glu Tyr Glu Met Gly Gln Ser Leu Ala Gln
 20 25 30
 Thr Ile Leu Phe His Asn Ser Val Asp Val Phe Gln Leu Asp Lys Asn
 35 40 45
 Val Ser Ile Val Glu Met Lys Ile Pro Gln Ser Trp Ala Gly Gln Ser
 50 55 60
 Leu Ser Lys Leu Asp Leu Arg Gly Lys Tyr Asn Leu Asn Ile Leu Gly
 65 70 75 80
 Phe Arg Glu Gln Glu Asn Ser Pro Leu Asp Val Glu Phe Gly Pro Asp
 85 90 95
 Asp Leu Leu Lys Ala Asp Thr Tyr Ile Leu Ala Val Ile Asn Asn Gln
 100 105 110
 Tyr Leu Asp Thr Leu
 115

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGACGGGTCT CAGGATCAGA CTCAGGAAAT CGCTGAGTGT TTAGCTAGCA AGTATCCTAA 60
 TATCGTTAGA GCCATCTATC AGGAAAATAA ATGCCATGGC GGTGCGGTCA ATCGTGGCTT 120
 GGTAGAGGCT TCTGGGCGCT ATTTTAAAGT AGTTGACAGT GATGACTGGG TGGATCCTCG 180
 TGCCTACTTG AAAATTCTTG AACTTGCAG GAACTTGAGA GCAAAGGTCA AGAGGTGGAT 240
 GTCTTTG 247

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Gly Ser Gln Asp Gln Thr Gln Glu Ile Ala Glu Cys Leu Ala Ser
 1 5 10 15
 Lys Tyr Pro Asn Ile Val Arg Ala Ile Tyr Gln Glu Asn Lys Cys His
 20 25 30
 Gly Gly Ala Val Asn Arg Gly Leu Val Glu Ala Ser Gly Arg Tyr Phe

(2) INFORMATION FOR SEO ID NO: 131:

(A) LENGTH: 1744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

TAGAGGCTTT	GCCAAATGGT	GGGAAGGGCA	CGAGCGTCGA	AAAGAGGAAC	GCTTTGTCAA	60
ACAAGAAGAA	AAAGCTCGCC	AAAAGGCTGA	GAAAGAGGCT	AGATTAGAAC	AAGAAGAGAC	120
TGAAAAAGCC	TTACTCGATT	TGCCTCCTGT	TGATATGGAA	ACGGGTGAAA	TTCTGACAGA	180
GGAAGCTGTT	CAAAATCTTC	CACCTATTCC	AGAAGAAAAG	TGGGTGGAAC	CAGAAATCAT	240
CCTGCCTCAA	GCTGAACTTA	AATTCCTTGA	ACAGGAAGAT	GACTCAGATG	ACGAAGATGT	300
TCAGGTCGAT	TTTTCAGCCA	AAGAAGCCCT	TGAATACAAA	CTTCCAAGCT	TACAACTCTT	360
TGCACCAGAT	AAACCAAAAG	ATCAGTCTAA	AGAGAAGAAA	ATTGTCAGAG	AAAATATCAA	420
AATCTTAGAA	GCAACCTTTG	CTAGCTTTGG	TATTAAAGGTA	ACAGTTGAAC	GGGCCGAAAT	480
TGGGCCATCA	GTGACCAAGT	ATGAAGTCAA	GCCGGCTGTT	GGTGTAAAGG	TCAACCGCAT	540
TTCCAATCTA	TCAGATGACC	TCGCTCTAGC	CTTGGCTGCC	AAAGATGTCC	GGATTGAAGC	600
ACCAATCCCT	GGGAAATCCC	TAATCGGAAT	TGAAGTGCCC	AACTCCGATA	TTGCCACTGT	660
ATCTTTCCGA	GAACATATGG	AACAATCGCA	AACGAAAGCA	GAAATTTTCT	TGGAAATTCC	720
TTTAGGGAAG	GCTGTTAATG	GAACCGCAAG	AGCTTTTGAC	CTTCTAAAA	TGCCCCACTT	780
GCTAGTTGCA	GTTTCAACGG	GTTTCAGGGAA	GTCAGTAGCA	GTTAACGGCA	TTATTGCTAG	840
CATTCTCATG	AAGGCGAGAC	CAGATCAAGT	TAAATTTATG	ATGGTCGATC	CCAAGATGGT	900
TGAGTTATCT	GTTTACAATG	ATATTCCCCA	CCTCTTGATT	CCAGTCGTGA	CCAATCCACG	960
CAAAGCCAGC	AAGGCTCTGC	AAAAGGTTGT	GGATGAAAATG	GAAAACCGTT	ATGAACTCTT	1020
TGCCAAGGTG	GGAGTTTCGA	ATATTGCAGG	TTTAAATGCC	AAGGTAGAAG	AGTTCAATTC	1080
CCAGTCTGAG	TACAAGCAAA	TTCCGCTACC	ATTCATTGTC	GTGATTGTGG	ATGAGTTGGC	1140
TGACCTCATG	ATGGTGGCCA	GCAAGGAAGT	GGAAGATGCT	ATCATCCGTC	TTGGGCAGAA	1200

GGCGCGTGCT GCAGGTATCC ACATGATTCT TGCAACTCAG CGTCCATCTG TTGATGTCAT 1260
 CTCTGGTTTG ATTAAGGCCA ATGTTCCATC TCGTGTAGCA TTTGCGGTTT CATCAGGAAC 1320
 AGACTCCCGT ACGATTTTGG ATGAAAATGG AGCAGAAAAA CTTCTTGGTC GAGGAGACAT 1380
 GCTCTTTAAA CCGATTGATG AAAATCATCC AGTTCGTCTC CAAGGCTCCT TTATCTCGGA 1440
 TGACGATGTT GAGCGCATTG TGAAC TTCAT CAAGACTCAG GCAGATGCAG ACTACGATGA 1500
 GAGTTTTGAT CCAGGTGAGG TTTCTGAAAA TGAAGGAGAA TTTTCGGATG GAGATGCTGG 1560
 TGGTGATCCG CTTTTTGAAG AAGCTAAGTC TTTGGTTATC GAAACACAGA AAGCCAGTGC 1620
 GTCTATGATT CAGCGTCGTT TATCAGTTGG ATTTAACCGT GCGACCCGTC TCATGGAAGA 1680
 ACTGGAGATA GCAGGTGTCA TCGGTCCAGC TGAAGGTACC AAACCTCGAA AAGTGTTACA 1740
 ACAA 1744

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 581 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Arg	Gly	Phe	Ala	Lys	Trp	Trp	Glu	Gly	His	Glu	Arg	Arg	Lys	Glu	Glu	1	5	10	15
Arg	Phe	Val	Lys	Gln	Glu	Glu	Lys	Ala	Arg	Gln	Lys	Ala	Glu	Lys	Glu	20	25	30	
Ala	Arg	Leu	Glu	Gln	Glu	Glu	Thr	Glu	Lys	Ala	Leu	Leu	Asp	Leu	Pro	35	40	45	
Pro	Val	Asp	Met	Glu	Thr	Gly	Glu	Ile	Leu	Thr	Glu	Glu	Ala	Val	Gln	50	55	60	
Asn	Leu	Pro	Pro	Ile	Pro	Glu	Glu	Lys	Trp	Val	Glu	Pro	Glu	Ile	Ile	65	70	75	80
Leu	Pro	Gln	Ala	Glu	Leu	Lys	Phe	Pro	Glu	Gln	Glu	Asp	Asp	Ser	Asp	85	90	95	
Asp	Glu	Asp	Val	Gln	Val	Asp	Phe	Ser	Ala	Lys	Glu	Ala	Leu	Glu	Tyr	100	105	110	
Lys	Leu	Pro	Ser	Leu	Gln	Leu	Phe	Ala	Pro	Asp	Lys	Pro	Lys	Asp	Gln	115	120	125	
Ser	Lys	Glu	Lys	Lys	Ile	Val	Arg	Glu	Asn	Ile	Lys	Ile	Leu	Glu	Ala	130	135	140	
Thr	Phe	Ala	Ser	Phe	Gly	Ile	Lys	Val	Thr	Val	Glu	Arg	Ala	Glu	Ile	145	150	155	160

Asp Tyr Asp Glu Ser Phe Asp Pro Gly Glu Val Ser Glu Asn Glu Gly
 500 505 510
 Glu Phe Ser Asp Gly Asp Ala Gly Gly Asp Pro Leu Phe Glu Glu Ala
 515 520 525
 Lys Ser Leu Val Ile Glu Thr Gln Lys Ala Ser Ala Ser Met Ile Gln
 530 535 540
 Arg Arg Leu Ser Val Gly Phe Asn Arg Ala Thr Arg Leu Met Glu Glu
 545 550 555 560
 Leu Glu Ile Ala Gly Val Ile Gly Pro Ala Glu Gly Thr Lys Pro Arg
 565 570 575
 Lys Val Leu Gln Gln
 580

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TCAAAAAGAG AAGGAAACT TGGTTATTGC TGGGAAAATA GGTCCAGAAC CAGAAATTTT	60
GGCCAATATG TATAAGTTGC TGATTGAAGA AAATACCAGC ATGACTGCGA CTGTTAAACC	120
GAATTTTGGG AAGACAAGCT TCCTTTATGA AGCTCTGAAA AAAGGCGATA TTGACATCTA	180
TCCTGAATTT ACTGGTACGG TGA CTGAAAG TTTGCTTCAA CCATCACCCA AGGTGAGTCA	240
TGAACCAGAA CAGGTTTATC AGGTGGCGCG TGATGGCATT GCTAAGCAGG ATCATCTAGC	300
CTATCTCAAA CCCATGTCTT ATCAAAACAC CTATGCTGTA GCTGTTCCGA AAAAGATTGC	360
TCAAGAATAT GGCTTGAAGA CCATTTTCTG CTTGAAAAAA GTGGAAGGGC AGTTGAAGGC	420
AGGTTTTTACA CTCGAGTTTA ACGACCGTGA AGATGGAAAT AAGGGCTTGC AATCAATGTA	480
TGGTCTCAAT CTCAATGTAG CGACCATTGA GCCAGCCCTT CGCTATCAGG CTATTTCAGTC	540
AGGGGATATT CAAATCACGG ATGCCTATTC GACTGATGCG GAATTGGAGC GTTATGATTT	600
ACAGGTCTTG GAAGATGACA AGCAACTCTT CCCACCTTAT CAAGGGGCTC CACTCATGAA	660
AGAAGCTCTT CTCAAGAAAC ACCCAGAGTT GGAAAGAGTT CTTAATACAT TGGCTGGTAA	720
GATTACAGAA AGCCAGATGA GCCAGCTCAA CTACCAAGTC GGTGTTGAAG GCAAGTCAGC	780
AAAGCAAGTA GCCAAGGAGT TTCTCCAAGA ACAAGGTTTG TTGAAGAAA	829

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Gln	Lys	Glu	Lys	Glu	Asn	Leu	Val	Ile	Ala	Gly	Lys	Ile	Gly	Pro	Glu	1	5	10	15
Pro	Glu	Ile	Leu	Ala	Asn	Met	Tyr	Lys	Leu	Leu	Ile	Glu	Glu	Asn	Thr	20	25	30	
Ser	Met	Thr	Ala	Thr	Val	Lys	Pro	Asn	Phe	Gly	Lys	Thr	Ser	Phe	Leu	35	40	45	
Tyr	Glu	Ala	Leu	Lys	Lys	Gly	Asp	Ile	Asp	Ile	Tyr	Pro	Glu	Phe	Thr	50	55	60	
Gly	Thr	Val	Thr	Glu	Ser	Leu	Leu	Gln	Pro	Ser	Pro	Lys	Val	Ser	His	65	70	75	80
Glu	Pro	Glu	Gln	Val	Tyr	Gln	Val	Ala	Arg	Asp	Gly	Ile	Ala	Lys	Gln	85	90	95	
Asp	His	Leu	Ala	Tyr	Leu	Lys	Pro	Met	Ser	Tyr	Gln	Asn	Thr	Tyr	Ala	100	105	110	
Val	Ala	Val	Pro	Lys	Lys	Ile	Ala	Gln	Glu	Tyr	Gly	Leu	Lys	Thr	Ile	115	120	125	
Ser	Asp	Leu	Lys	Lys	Val	Glu	Gly	Gln	Leu	Lys	Ala	Gly	Phe	Thr	Leu	130	135	140	
Glu	Phe	Asn	Asp	Arg	Glu	Asp	Gly	Asn	Lys	Gly	Leu	Gln	Ser	Met	Tyr	145	150	155	160
Gly	Leu	Asn	Leu	Asn	Val	Ala	Thr	Ile	Glu	Pro	Ala	Leu	Arg	Tyr	Gln	165	170	175	
Ala	Ile	Gln	Ser	Gly	Asp	Ile	Gln	Ile	Thr	Asp	Ala	Tyr	Ser	Thr	Asp	180	185	190	
Ala	Glu	Leu	Glu	Arg	Tyr	Asp	Leu	Gln	Val	Leu	Glu	Asp	Asp	Lys	Gln	195	200	205	
Leu	Phe	Pro	Pro	Tyr	Gln	Gly	Ala	Pro	Leu	Met	Lys	Glu	Ala	Leu	Leu	210	215	220	
Lys	Lys	His	Pro	Glu	Leu	Glu	Arg	Val	Leu	Asn	Thr	Leu	Ala	Gly	Lys	225	230	235	240
Ile	Thr	Glu	Ser	Gln	Met	Ser	Gln	Leu	Asn	Tyr	Gln	Val	Gly	Val	Glu	245	250	255	
Gly	Lys	Ser	Ala	Lys	Gln	Val	Ala	Lys	Glu	Phe	Leu	Gln	Glu	Gln	Gly	260	265	270	
Leu	Leu	Lys	Lys													275			

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```

ACGTTCTATT GAGGACCACT TTGATTCAAA CTTCAATTG GAATATAACC TCAAAGAAAA      60
AGGGAAAACA GATCTTTTGA AGCTAGTTGA TAAACAACCT GACATGCGTC TGCATTTTAT      120
CCGCCAAACT CATCCACGCG GTCTCGGAGA TGCTGTTTTG CAAGCCAAGG CTTTCGTCGG      180
AAATGAACCT TTTGTCGTTA TGCTTGGTGA TGACTTGATG GATATCACAG ACGAAAAGGC      240
TGTTCCACTT ACCAAACAAC TCATGGATGA CTACGAGCGT ACCCACGCGT CTACTATCGC      300
TGTCATGCCA GTCCCTCATG ACGAAGTATC TGCTTACGGG GTTATTGCTC CGCAAGGCCA      360
AGGAAAAGAT GGTCTTTACA GTGTTGAAAC CTTTGTTGAA AAACCAGCTC CAGAGGACGC      420
TCCTAGCGAC CTTGCTATTA TCGGACGCTA CCTCCTCACG CCTGAAATTT TTGAGATTCT      480
CGAAAAGCAA GCTCCAGGTG CAGGAAATGA AATTCAGCTG ACAGATGCAA TCGACACCCT      540
CAATAAAACA CAACGTGTAT TTGCTCGTGA GTTCAAAGGG GCTCGTTACG ATGTCGGAGA      600
CAAGTTTGGC TTCATGAAAA CATCCATCGA CTACGCCCTC AAACACCCAC AAGTCAAAGA      660
TGATTTGAAG AATTACCTCA TCCAAC TTGG AAAAGAATTG ACTGAGAAGG AA      712

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(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

Arg Ser Ile Glu Asp His Phe Asp Ser Asn Phe Glu Leu Glu Tyr Asn
1           5           10           15
Leu Lys Glu Lys Gly Lys Thr Asp Leu Leu Lys Leu Val Asp Lys Thr
          20           25           30
Thr Asp Met Arg Leu His Phe Ile Arg Gln Thr His Pro Arg Gly Leu
          35           40           45
Gly Asp Ala Val Leu Gln Ala Lys Ala Phe Val Gly Asn Glu Pro Phe
          50           55           60
Val Val Met Leu Gly Asp Asp Leu Met Asp Ile Thr Asp Glu Lys Ala
          65           70           75           80

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Val Pro Leu Thr Lys Gln Leu Met Asp Asp Tyr Glu Arg Thr His Ala
85 90 95

Ser Thr Ile Ala Val Met Pro Val Pro His Asp Glu Val Ser Ala Tyr
100 105 110

Gly Val Ile Ala Pro Gln Gly Glu Gly Lys Asp Gly Leu Tyr Ser Val
115 120 125

Glu Thr Phe Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Asp Leu
130 135 140

Ala Ile Ile Gly Arg Tyr Leu Leu Thr Pro Glu Ile Phe Glu Ile Leu
145 150 155 160

Glu Lys Gln Ala Pro Gly Ala Gly Asn Glu Ile Gln Leu Thr Asp Ala
165 170 175

Ile Asp Thr Leu Asn Lys Thr Gln Arg Val Phe Ala Arg Glu Phe Lys
180 185 190

Gly Ala Arg Tyr Asp Val Gly Asp Lys Phe Gly Phe Met Lys Thr Ser
195 200 205

Ile Asp Tyr Ala Leu Lys His Pro Gln Val Lys Asp Asp Leu Lys Asn
210 215 220

Tyr Leu Ile Gln Leu Gly Lys Glu Leu Thr Glu Lys Glu
225 230 235

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGCTCAAAAT ACCAGAGGTG TTCAGCTAAT CGAGCACGTT TCTCCTCAAA TGTGAAAGC 60

CCAATTGGAG AGTGTCTTTT CTGATATTCC ACCTCAGGCT GTAAAACTG GAATGTTGGC 120

TACTACTGAA ATCATGGAAA TCATCCAACC CTATCTTAAA AACTGGATT GTCCCTATGT 180

CCTTGATCCT GTTATGGTTG CTACAAGTGG AGATGCCTTG ATTGACTCAA ATGCTAGAGA 240

CTATCTCAAA ACAAACTTAC TACCTCTAGC AACTATTATT ACGCCAAATC TTCCTGAAGC 300

AGAAGAGATT GTTGGTTTTT CAATCCATGA CCCCGAAGAC ATGCAGCGTG CTGGTCGCCT 360

GATTTTAAAA GAATTTGGTC CTCAGTCTGT GGTTATCAAA GCGGACATC TCAAAGGTGG 420

TGCTAAAGAT TTCTCTTTA CCAAGAATGA ACAATTTGTC TGGGAAAGCC CACGAATTCA 480

AACCTGTCAC ACCCATGGTA CT 502

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ala	Gln	Asn	Thr	Arg	Gly	Val	Gln	Leu	Ile	Glu	His	Val	Ser	Pro	Gln	1	5	10	15
Met	Leu	Lys	Ala	Gln	Leu	Glu	Ser	Val	Phe	Ser	Asp	Ile	Pro	Pro	Gln	20	25	30	
Ala	Val	Lys	Thr	Gly	Met	Leu	Ala	Thr	Thr	Glu	Ile	Met	Glu	Ile	Ile	35	40	45	
Gln	Pro	Tyr	Leu	Lys	Lys	Leu	Asp	Cys	Pro	Tyr	Val	Leu	Asp	Pro	Val	50	55	60	
Met	Val	Ala	Thr	Ser	Gly	Asp	Ala	Leu	Ile	Asp	Ser	Asn	Ala	Arg	Asp	65	70	75	80
Tyr	Leu	Lys	Thr	Asn	Leu	Leu	Pro	Leu	Ala	Thr	Ile	Ile	Thr	Pro	Asn	85	90	95	
Leu	Pro	Glu	Ala	Glu	Glu	Ile	Val	Gly	Phe	Ser	Ile	His	Asp	Pro	Glu	100	105	110	
Asp	Met	Gln	Arg	Ala	Gly	Arg	Leu	Ile	Leu	Lys	Glu	Phe	Gly	Pro	Gln	115	120	125	
Ser	Val	Val	Ile	Lys	Gly	Gly	His	Leu	Lys	Gly	Gly	Ala	Lys	Asp	Phe	130	135	140	
Leu	Phe	Thr	Lys	Asn	Glu	Gln	Phe	Val	Trp	Glu	Ser	Pro	Arg	Ile	Gln	145	150	155	160
Thr	Cys	His	Thr	His	Gly	Thr	165												

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 805 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

AATTGTACAA	TTAGAAAAAG	ATAGCAAATC	AGACAAAGAA	CAAGTTGATA	AACTATTTGA	60
ATCATTGTGAT	GCATCTTCAG	ATGAATCTAT	TTCTAAATTA	AAAGAACTAT	CTGAAACTTC	120
ACTTAAAACC	GATGCAGGTA	AAGACTATCT	TAATAACAAA	GTCAAAGAAT	CATCTAAAGC	180
AATTGTAGAT	TTTCATTTCG	AAAAAGGTTT	GGCTTATGAT	GTTAAAGATT	CAGATGACAA	240

ATTTAAAGAT AAAGCAACTC TTGAAACAAA TGTAAGAGAA ATTACAAAAC AAATTGATTT 300
 TATCAAAAAA GTTGATGAAA CTTTAAACA AGAGAATTTG GAAGAACTC TTAAATCTCT 360
 AAATGATCTT GTTGATAAAT ATCAAAAACA AATCGAACTT TTGAAGAAAG AAGAAGAAAA 420
 AGCTGCTGAA AAAGCTGCTG AAAAAGCAAA GGAATCTTCT AGTCAAAGTA ATTCTTCTGG 480
 TAGTGCTTCT AATGAGTCTT ATAATGGATC TTCCAATTCA AATGTAGATT ATAGTTCATC 540
 TGAACAAACT AATGGATATT CAAATAATTA TGGCGGTCAA GATTATTCTG GTTCAGGAGA 600
 TAGTTCAACA AATGGTGGAT CATCAGAACA ATATTCATCT AGCAATTCAA ACAGCGGAGC 660
 AAATAATGTC TACAGATATA AAGGCACTGG TGCTGACGGC TATCAAAGAT ACTACTACAA 720
 AGATCATAAT AATGGAGATG TGTATGATG CGATGGAAAT TACCTTGGGA ACTTTGGTGG 780
 CGGCATTGCA GAACCTAGTC AACGC 805

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 268 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile	Val	Gln	Leu	Glu	Lys	Asp	Ser	Lys	Ser	Asp	Lys	Glu	Gln	Val	Asp	1	5	10	15
Lys	Leu	Phe	Glu	Ser	Phe	Asp	Ala	Ser	Ser	Asp	Glu	Ser	Ile	Ser	Lys	20	25	30	
Leu	Lys	Glu	Leu	Ser	Glu	Thr	Ser	Leu	Lys	Thr	Asp	Ala	Gly	Lys	Asp	35	40	45	
Tyr	Leu	Asn	Asn	Lys	Val	Lys	Glu	Ser	Ser	Lys	Ala	Ile	Val	Asp	Phe	50	55	60	
His	Leu	Gln	Lys	Gly	Leu	Ala	Tyr	Asp	Val	Lys	Asp	Ser	Asp	Asp	Lys	65	70	75	80
Phe	Lys	Asp	Lys	Ala	Thr	Leu	Glu	Thr	Asn	Val	Lys	Glu	Ile	Thr	Lys	85	90	95	
Gln	Ile	Asp	Phe	Ile	Lys	Lys	Val	Asp	Glu	Thr	Phe	Lys	Gln	Glu	Asn	100	105	110	
Leu	Glu	Glu	Thr	Leu	Lys	Ser	Leu	Asn	Asp	Leu	Val	Asp	Lys	Tyr	Gln	115	120	125	
Lys	Gln	Ile	Glu	Leu	Leu	Lys	Lys	Glu	Glu	Glu	Lys	Ala	Ala	Glu	Lys	130	135	140	
Ala	Ala	Glu	Lys	Ala	Lys	Glu	Ser	Ser	Ser	Gln	Ser	Asn	Ser	Ser	Gly	145	150	155	160

(2) INFORMATION FOR SEQ ID NO: 141:

(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCTGACCAAG	CAAAAAGAAG	CAGTCAATGA	CAAAGGAAAA	GCAGCTGTTG	TTAAGGTGGT	60
GGAAAGCCAG	GCAGAACTTT	ATAGCTTAGA	AAAGAATGAA	GATGCTAGCC	TAAGAAAGTT	120
ACAAGCAGAT	GGACGCATCA	CGGAAGAACA	GGCTAAAGCT	TATAAAGAAT	ACAATGATAA	180
AAATGGAGGA	GCAAATCGTA	AAGTCAATGA	T			211

(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Leu Thr Lys Gln Lys Glu Ala Val Asn Asp Lys Gly Lys Ala Ala Val
1          5          10          15
Val Lys Val Val Glu Ser Gln Ala Glu Leu Tyr Ser Leu Glu Lys Asn
          20          25          30
Glu Asp Ala Ser Leu Arg Lys Leu Gln Ala Asp Gly Arg Ile Thr Glu
          35          40          45

```


(2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

GGGACAAATT CAAAAAATA GGCAAGAGGA AGCAAAAATC TTGCAAAAGG AAGAAGTCTT      60
GAGGGTAGCT AAGATGGCCC TGCAGACGGG GCAAAATCAG GTAAGCATCA ACGGAGTTGA      120
GATTCAGGTA TTTTCTAGTG AAAAAGGATT GGAGGTCTAC CATGGTTCAG AACAGTTGTT      180
GGCAATCAAA GAGCCA                                          196

```

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Gly Gln Ile Gln Lys Asn Arg Gln Glu Glu Ala Lys Ile Leu Gln Lys
1           5           10           15
Glu Glu Val Leu Arg Val Ala Lys Met Ala Leu Gln Thr Gly Gln Asn
          20           25           30
Gln Val Ser Ile Asn Gly Val Glu Ile Gln Val Phe Ser Ser Glu Lys
          35           40           45
Gly Leu Glu Val Tyr His Gly Ser Glu Gln Leu Leu Ala Ile Lys Glu
50           55           60
Pro
65

```

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```

TCGCTACCAG CAACAAAGCG AGCAAAAGGA GTGGCTCTTG TTTGTGGACC AACTTGAGGT      60

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AGAATTAGAC CGTTCGCAGT TCGAAAAAGT AGAAGGCAAT CGCCTATACA TGAAGCAAGA 120
 TGGCAAGGAC ATCGCCATCG GTAAGTCAAA GTCAGATGAT TTCCGTAAAA CGAATGCTCG 180
 TGGTCGAGGT TATCAGCCTA TGGTTTATGG ACTCAAATCT GTACGGATTA CAGAGGACAA 240
 TCAACTGGTT CGCTTTCATT TCCAGTTCCA AAAAGGCTTA GAAAGGGAGT TCATCTATCG 300
 TGTGGAAAAA GAAAAAAGT 319

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Arg Tyr Gln Gln Gln Ser Glu Gln Lys Glu Trp Leu Leu Phe Val Asp
 1 5 10 15
 Gln Leu Glu Val Glu Leu Asp Arg Ser Gln Phe Glu Lys Val Glu Gly
 20 25 30
 Asn Arg Leu Tyr Met Lys Gln Asp Gly Lys Asp Ile Ala Ile Gly Lys
 35 40 45
 Ser Lys Ser Asp Asp Phe Arg Lys Thr Asn Ala Arg Gly Arg Gly Tyr
 50 55 60
 Gln Pro Met Val Tyr Gly Leu Lys Ser Val Arg Ile Thr Glu Asp Asn
 65 70 75 80
 Gln Leu Val Arg Phe His Phe Gln Phe Gln Lys Gly Leu Glu Arg Glu
 85 90 95
 Phe Ile Tyr Arg Val Glu Lys Glu Lys Ser
 100 105

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GAACCGACAA GTCGCCCCACT ATCAAGACTA TGCTTTGAAT AAAGAAAAAT TGGTTGCTTT 60
 TGCTATGGCT AAACGAACCA AAGATAAGGT TGAGCAAGAA AGTGGGGAAC AGTTTTTTTAA 120
 TCTAGGTCAG GTAAGCTATC AAAACAAGAA AACTGGCTTA GTGACGAGGG TTCGTACGGA 180
 TAAGAGCCAA TATGAGTTTC TGTTCCTTC AGTCAAAATC AAAGAAGAGA AAAGAGATAA 240

AAAGGAAGAG GTAGCGACCG ATTCAAGCGA AAAAGTGGAG AAGAAAAAAT CAGAAGAGAA 300
GCCTGAAAAG AAAGAGAATT CA 322

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Asn Arg Gln Val Ala His Tyr Gln Asp Tyr Ala Leu Asn Lys Glu Lys
1 5 10 15
Leu Val Ala Phe Ala Met Ala Lys Arg Thr Lys Asp Lys Val Glu Gln
20 25 30
Glu Ser Gly Glu Gln Phe Phe Asn Leu Gly Gln Val Ser Tyr Gln Asn
35 40 45
Lys Lys Thr Gly Leu Val Thr Arg Val Arg Thr Asp Lys Ser Gln Tyr
50 55 60
Glu Phe Leu Phe Pro Ser Val Lys Ile Lys Glu Glu Lys Arg Asp Lys
65 70 75 80
Lys Glu Glu Val Ala Thr Asp Ser Ser Glu Lys Val Glu Lys Lys Lys
85 90 95
Ser Glu Glu Lys Pro Glu Lys Lys Glu Asn Ser
100 105

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GGTTGTCGGC TGGCAATATA TCCCGTTTCC ATCTAAAGGT AGTACAATTG GTCCTTACCC 60
AAATGGTATC AGATTAGAAG GTTTTCCAAA GTCAGAGTGG TACTACTTCG ATAAAAATGG 120
AGTGCTACAA GAGTTTGTTG GTTGGAAAAC ATTAGAGATT AAAACTAAAG ACAGTGTTGG 180
AAGAAAGTAC GGGGAAAAAC GTGAAGATTC AGAAGATAAA GAAGAGAAGC GTTATTATAC 240
GAACTATTAC TTTAATCAAA ATCATTCTTT AGAGACAGGT TGGCTTTATG ATCAGTCTAA 300
CTGGTATTAT CTAGCTAAGA CGGAAATTAA TGGAGAAAAC TACCTTGGTG GTGAAAGACG 360

TCGGGGGTGG ATAAACGATG ATTCGACTTG GTACTACCTA GATCCAACAA CTGGTATTAT 420
 GCAAACAGGT TGGCAATATC TAGGTAATAA GTGGTACTAC CTCCGTTCTT CAGGAGCAAT 480
 GGCCACTGGC TGGTATCAGG AAGGTACCAC TTGGTATTAT TTAGACCACC CAAATGGCGA 540
 TATGAAAACA GGTGGCAAAA ACCTTGGGAA CAAATGGTAC TATCTCCGTT CATCAGGAGC 600
 TATGGCAACT GGTGGTATC AAGATGGTTC AACTTGGTAC TACCTAAATG CAGGTAATGG 660
 AGACATGAAG ACAGGTTGGT TCCAGGTCAA TGGCAACTGG TACTATGCTT ATAGCTCAGG 720
 TGCTTTGGCA GTGAATACGA CCGTAGATGG CTATTCTGTC AACTATAATG GCGAATGGGT 780
 TCGG 784

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Val	Val	Gly	Trp	Gln	Tyr	Ile	Pro	Phe	Pro	Ser	Lys	Gly	Ser	Thr	Ile	1	5	10	15
Gly	Pro	Tyr	Pro	Asn	Gly	Ile	Arg	Leu	Glu	Gly	Phe	Pro	Lys	Ser	Glu	20	25	30	
Trp	Tyr	Tyr	Phe	Asp	Lys	Asn	Gly	Val	Leu	Gln	Glu	Phe	Val	Gly	Trp	35	40	45	
Lys	Thr	Leu	Glu	Ile	Lys	Thr	Lys	Asp	Ser	Val	Gly	Arg	Lys	Tyr	Gly	50	55	60	
Glu	Lys	Arg	Glu	Asp	Ser	Glu	Asp	Lys	Glu	Glu	Lys	Arg	Tyr	Tyr	Thr	65	70	75	80
Asn	Tyr	Tyr	Phe	Asn	Gln	Asn	His	Ser	Leu	Glu	Thr	Gly	Trp	Leu	Tyr	85	90	95	
Asp	Gln	Ser	Asn	Trp	Tyr	Tyr	Leu	Ala	Lys	Thr	Glu	Ile	Asn	Gly	Glu	100	105	110	
Asn	Tyr	Leu	Gly	Gly	Glu	Arg	Arg	Ala	Gly	Trp	Ile	Asn	Asp	Asp	Ser	115	120	125	
Thr	Trp	Tyr	Tyr	Leu	Asp	Pro	Thr	Thr	Gly	Ile	Met	Gln	Thr	Gly	Trp	130	135	140	
Gln	Tyr	Leu	Gly	Asn	Lys	Trp	Tyr	Tyr	Leu	Arg	Ser	Ser	Gly	Ala	Met	145	150	155	160
Ala	Thr	Gly	Trp	Tyr	Gln	Glu	Gly	Thr	Thr	Trp	Tyr	Tyr	Leu	Asp	His	165	170	175	
Pro	Asn	Gly	Asp	Met	Lys	Thr	Gly	Trp	Gln	Asn	Leu	Gly	Asn	Lys	Trp				

260
180
185
190
195
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205
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225
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235
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245
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255
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260
180 185 190
Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp
195 200 205
Gly Ser Thr Trp Tyr Tyr Leu Asn Ala Gly Asn Gly Asp Met Lys Thr
210 215 220
Gly Trp Phe Gln Val Asn Gly Asn Trp Tyr Tyr Ala Tyr Ser Ser Gly
225 230 235 240
Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Ser Val Asn Tyr Asn
245 250 255
Gly Glu Trp Val Arg
260

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GGCCAAATCA GAATGGGTAG AAGACAAGGG AGCCTTTTAT TATCTTGACC AAGATGGAAA 60
GATGAAAAGA AATGCTTGGG TAGGAACTTC CTATGTTGGT GCAACAGGTG CCAAAGTAAT 120
AGAAGACTGG GTCTATGATT CTCAATACGA TGCTTGGTTT TATATCAAAG CAGATGGACA 180
GCACGCAGAG AAAGAATGGC TCCAAATTAA AGGGAAGGAC TATTATTTC AATCCGGTGG 240
TTATCTACTG ACAAGTCAGT GGATTAATCA AGCTTATGTG AATGCTAGTG GTGCCAAAGT 300
ACAGCAAGGT TGGCTTTTTG ACAAACAATA CCAATCTTGG TTTTACATCA AAGAAAATGG 360
AAACTATGCT GATAAAGAAT GGATTTTCGA GAATGGTCAC TATTATTATC TAAAATCCGG 420
TGGCTACATG GCAGCCAATG AATGGATTTG GGATAAGGAA TCTTGTTTTT ATCTCAAATT 480
TGATGGGAAA ATGGCTGAAA AAGAATGGGT CTACGATTCT CATAGTCAAG CTTGGTACTA 540
CTTCAAATCC GGTGGTTACA TGACAGCCAA TGAATGGATT TGGGATAAGG AATCTTGTTT 600
TTATCTCAAA TCTGATGGGA AAATAGCTGA AAAAGAATGG GTCTACGATT CTCATAGTCA 660
AGCTTGGTAC TACTTCAAAT CCGGTGGTTA CATGACAGCC AATGAATGGA TTTGGGATAA 720
GGAATCTTGG TTTTACCTCA AATCTGATGG GAAAATAGCT GAAAAAGAAT GGGTCTACGA 780
TTCTCATAGT CAAGCTTGGT ACTACTTCAA ATCTGGTGGC TACATGGCGA AAAATGAGAC 840
AGTAGATGGT TATCAGCTTG GAAGCGATGG TAAATGGCTT GGAGGAAAAA CTACAAATGA 900
AAATGCTGCT TACTATCAAG TAGTGCCTGT TACAGCCAAT GTTTATGATT CAGATGGTGA 960
AAAGCTTTCC TATATATCGC AAGGTAGTGT CGTATGGCTA GATAAGGATA GAAAAAGTGA 1020

TGACAAGCGC TTGGCTATTA CTATTTCTGG TTTGTCAGGC TATATGAAAA CAGAAGATTT 1080
 ACAAGCGCTA GATGCTAGTA AGGACTTTAT CCCTTATTAT GAGAGTGATG GCCACCGTTT 1140
 TTATCACTAT GTGGCTCAGA ATGCTAGTAT CCCAGTAGCT TCTCATCTTT CTGATATGGA 1200
 AGTAGGCAAG AAATATTATT CGGCAGATGG CCTGCATTTT GATGGTTTTA AGCTTGAGAA 1260
 TCCCTTCCTT TTCAAAGATT TAACAGAGGC TACAAACTAC AGTGCTGAAG AATTGGATAA 1320
 GGTATTTAGT TTGCTAAACA TTAACAATAG CCTTTTGGAG AACAAGGGCG CTACTTTTAA 1380
 GGAAGCCGAA GAACATTACC ATATCAATGC TCTTTATCTC CTTGCCCCATA GTGCCCTAGA 1440
 AAGTAACTGG GGAAGAAGTA AAATTGCCAA AGATAAGAAT AATTTCTTTG GCATTACAGC 1500
 CTATGATACG ACCCCTTACC TTTCTGCTAA GACATTTGAT GATGTGGATA AGGGAATTTT 1560
 AGGTGCAACC AAGTGGATTA AGGAAAATTA TATCGATAGG GGAAGAACTT TCCTTGAAAA 1620
 CAAGGCTTCT GGTATGAATG TGGAATATGC TTCAGACCCT TATTGGGGCG AAAAAATTGC 1680
 TAGTGTGATG ATGAAAATCA ATGAGAAG 1708

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 569 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Ala Lys Ser Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp
 1 5 10 15
 Gln Asp Gly Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val
 20 25 30
 Gly Ala Thr Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln
 35 40 45
 Tyr Asp Ala Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys
 50 55 60
 Glu Trp Leu Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly
 65 70 75 80
 Tyr Leu Leu Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser
 85 90 95
 Gly Ala Lys Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser
 100 105 110
 Trp Phe Tyr Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile
 115 120 125
 Phe Glu Asn Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala
 130 135 140

(2) INFORMATION FOR SEQ ID NO: 155:

(A) LENGTH: 946 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATTTCGAGAT	GATTCTGAAG	GATGGCAGTT	TGTCCAAGAA	AATGGTAGAA	CCTACTACAA	60
AAAGGGGGAT	CTAAAAGAAA	CCTACTGGAG	AGTGATAGAT	GGGAAGTACT	ATTATTTTGA	120
TCCTTTTATCC	GGAGAGATGG	TTGTCTGGCTG	GCAATATATA	CCTGCTCCAC	ACAAGGGGGT	180
TACGATTGGT	CCTTCTCCAA	GAATAGAGAT	TGCTCTTAGA	CCGATTGGT	TTTATTTTGG	240
TCAAGATGGT	GTATTACAAG	AATTTGTTGG	CAAGCAAGTT	TTAGAAGCAA	AAACTGCTAC	300
GAATACCAAC	AAACATCATG	GGGAAGAATA	TGATAGCCAA	GCAGAGAAAC	GAGTCTATTA	360
TTTTGAAGAT	CAGCGTAGTT	ATCATACTTT	AAAAACTGGT	TGGATTTATG	AAGAGGGTCA	420
TTGGTATTAT	TTACAGAAGG	ATGGTGGCTT	TGATTCTGCGC	ATCAACAGAT	TGACGGTTGG	480
AGAGCTAGCA	CGTGGTTGGG	TTAAGGATTA	CCCTCTTACG	TATGATGAAG	AGAAGCTAAA	540
AGCAGCTCCA	TGGTACTATC	TAAATCCAGC	AACTGGCATT	ATGCAAACAG	GTTGGCAATA	600
TCTAGGTAAT	AGATGGTACT	ACCTCCATTC	GTCAGGAGCT	ATGGCAACTG	GCTGGTATAA	660
GGAAGGCTCA	ACTTGGTACT	ATCTAGATGC	TGAAAATGGT	GATATGAGAA	CTGGCTGGCA	720
AAACCTTGGG	AACAAATGGT	ACTATCTCCG	TTCATCAGGA	GCTATGGCAA	CTGGTTGGTA	780
TCAGGAAAGT	TCGACTTGGT	ACTATCTAAA	TGCAAGTAAT	GGAGATATGA	AAACAGGCTG	840
GTTCCAAGTC	AATGGTAACT	GGTACTATGC	CTATGATTCA	GGTGCTTTAG	CTGTTAATAC	900
CACAGTAGGT	GGTTACTACT	TAAACTATAA	TGGTGAATGG	GTTAAG		946

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

Val Phe Ala Asp Asp Ser Glu Gly Trp Gln Phe Val Gln Glu Asn Gly
1           5           10           15
Arg Thr Tyr Tyr Lys Lys Gly Asp Leu Lys Glu Thr Tyr Trp Arg Val
20          25          30
Ile Asp Gly Lys Tyr Tyr Tyr Phe Asp Pro Leu Ser Gly Glu Met Val
35          40          45
Val Gly Trp Gln Tyr Ile Pro Ala Pro His Lys Gly Val Thr Ile Gly
50          55          60
Pro Ser Pro Arg Ile Glu Ile Ala Leu Arg Pro Asp Trp Phe Tyr Phe
65          70          75          80
Gly Gln Asp Gly Val Leu Gln Glu Phe Val Gly Lys Gln Val Leu Glu
85          90          95
Ala Lys Thr Ala Thr Asn Thr Asn Lys His His Gly Glu Glu Tyr Asp
100         105         110
Ser Gln Ala Glu Lys Arg Val Tyr Tyr Phe Glu Asp Gln Arg Ser Tyr
115         120         125
His Thr Leu Lys Thr Gly Trp Ile Tyr Glu Glu Gly His Trp Tyr Tyr
130         135         140
Leu Gln Lys Asp Gly Gly Phe Asp Ser Arg Ile Asn Arg Leu Thr Val
145         150         155         160
Gly Glu Leu Ala Arg Gly Trp Val Lys Asp Tyr Pro Leu Thr Tyr Asp
165         170         175
Glu Glu Lys Leu Lys Ala Ala Pro Trp Tyr Tyr Leu Asn Pro Ala Thr
180         185         190
Gly Ile Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Arg Trp Tyr Tyr
195         200         205
Leu His Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Lys Glu Gly Ser
210         215         220
Thr Trp Tyr Tyr Leu Asp Ala Glu Asn Gly Asp Met Arg Thr Gly Trp
225         230         235         240
Gln Asn Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met
245         250         255
Ala Thr Gly Trp Tyr Gln Glu Ser Ser Thr Trp Tyr Tyr Leu Asn Ala
260         265         270

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Ser Asn Gly Asp Met Lys Thr Gly Trp Phe Gln Val Asn Gly Asn Trp
 275 280 285

Tyr Tyr Ala Tyr Asp Ser Gly Ala Leu Ala Val Asn Thr Thr Val Gly
 290 295 300

Gly Tyr Tyr Leu Asn Tyr Asn Gly Glu Trp Val Lys
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1415 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTCGCTGCA AATGAACTG AAGTAGCAAA AACTTCGCAG GATACAACGA CAGCTTCAAG	60
TAGTTCAGAG CAAAATCAGT CTTCTAATAA AACGCAAACG AGCGCAGAAG TACAGACTAA	120
TGCTGCTGCC CACTGGGATG GGGATTATTA TGTAAGGAT GATGGTTCTA AAGCTCAAAG	180
TGAATGGATT TTTGACAAC TATAAAGGC TTGGTTTTAT ATTAATTCAG ATGGTCGTTA	240
CTCGCAGAAT GAATGGCATG GAAATTACTA CCTGAAATCA GGTGGATATA TGGCCCAAAA	300
CGAGTGGATC TATGACAGTA ATTACAAGAG TTGGTTTTAT CTCAAGTCAG ATGGGGCTTA	360
TGCTCATCAA GAATGGCAAT TGATTGGAAA TAAGTGGTAC TACTTCAAGA AGTGGGGTTA	420
CATGGCTAAA AGCCAATGGC AAGGAAGTTA TTTCTTGAAT GGTCAAGGAG CTATGATGCA	480
AAATGAATGG CTSCATGAT CCAGCCTATT CTGCTTATTT TTATCTAAAA TCCGATGGAA	540
CTTATGCTAA CCAAGAGTGG CAAAAGTGG GCGGCAAATG GTACTATTTT AAGAAGTGGG	600
GCTATATGGC TCGGAATGAG TGGCAAGGCA ACTACTATTT GACTGGAAGT GGTGCCATGG	660
CGACTGACGA AGTGATTATG GATGGTACTC GCTATATCTT TCGGCCTCT GGTGAGCTCA	720
AAGAAAAAAA AGATTGGAAT GTCGGCTGGG TTCACAGAGA TGGTAAGCGC TATTTCTTTA	780
ATAATAGAGA AGAACAAGTG GGAACCGAAC ATGCTAAGAA AGTCATTGAT ATTAGTGAGC	840
ACAATGGTCG TATCAATGAT TGGAAAAAGG TTATTGATGA GAACGAAGTG GATGGTGTCA	900
TTGTTCTGCT AGGTTATAGC GGTAAGAAG ACAAGGAATT GGCGCATAAC ATTAAGGAGT	960
TAAACCGTCT GGAATTCCT TATGGTGTCT ATCTCTATAC CTATGCTGAA AATGAGACCG	1020
ATGCTGAGAG TGACGCTAAA CAGACCATTG AACTTATAAA GAAATACAAT ATGAACCTGT	1080
CTTACCCTAT CTATTATGAT GTTGAGAATT GGGAATATGT AAATAAGAGC AAGAGAGCTC	1140
CAAGTGATAC AGGCACTTGG GTTAAAATCA TCAACAAGTA CATGGACACG ATGAAGCAGG	1200
CGGGTTATCA AAATGTGTAT GTCTATAGCT ATCGTAGTTT ATTACAGACG CGTTTAAAC	1260

ACCCAGATAT TTAAAAACAT GTAAACTGGG TAGCGGCCTA TACGAATGCT TTAGAATGGG 1320
 AAAACCCCTCA TTATTCAGGA AAAAAAGGTT GGCAATATAC CTCTTCTGAA TACATGAAAG 1380
 GAATCCAAGG GCGCGTAGAT GTCAGCGTTT GGTAT 1415

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Val	Ala	Ala	Asn	Glu	Thr	Glu	Val	Ala	Lys	Thr	Ser	Gln	Asp	Thr	Thr	1	5	10	15
Thr	Ala	Ser	Ser	Ser	Ser	Glu	Gln	Asn	Gln	Ser	Ser	Asn	Lys	Thr	Gln	20	25	30	
Thr	Ser	Ala	Glu	Val	Gln	Thr	Asn	Ala	Ala	Ala	His	Trp	Asp	Gly	Asp	35	40	45	
Tyr	Tyr	Val	Lys	Asp	Asp	Gly	Ser	Lys	Ala	Gln	Ser	Glu	Trp	Ile	Phe	50	55	60	
Asp	Asn	Tyr	Tyr	Lys	Ala	Trp	Phe	Tyr	Ile	Asn	Ser	Asp	Gly	Arg	Tyr	65	70	75	80
Ser	Gln	Asn	Glu	Trp	His	Gly	Asn	Tyr	Tyr	Leu	Lys	Ser	Gly	Gly	Tyr	85	90	95	
Met	Ala	Gln	Asn	Glu	Trp	Ile	Tyr	Asp	Ser	Asn	Tyr	Lys	Ser	Trp	Phe	100	105	110	
Tyr	Leu	Lys	Ser	Asp	Gly	Ala	Tyr	Ala	His	Gln	Glu	Trp	Gln	Leu	Ile	115	120	125	
Gly	Asn	Lys	Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Lys	Ser	130	135	140	
Gln	Trp	Gln	Gly	Ser	Tyr	Phe	Leu	Asn	Gly	Gln	Gly	Ala	Met	Met	Gln	145	150	155	160
Asn	Glu	Trp	Leu	Tyr	Asp	Pro	Ala	Tyr	Ser	Ala	Tyr	Phe	Tyr	Leu	Lys	165	170	175	
Ser	Asp	Gly	Thr	Tyr	Ala	Asn	Gln	Glu	Trp	Gln	Lys	Val	Gly	Gly	Lys	180	185	190	
Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Arg	Asn	Glu	Trp	Gln	195	200	205	
Gly	Asn	Tyr	Tyr	Leu	Thr	Gly	Ser	Gly	Ala	Met	Ala	Thr	Asp	Glu	Val	210	215	220	
Ile	Met	Asp	Gly	Thr	Arg	Tyr	Ile	Phe	Ala	Ala	Ser	Gly	Glu	Leu	Lys				

225		230		235		240
Glu Lys Lys Asp Leu Asn Val Gly Trp Val His Arg Asp Gly Lys Arg						
	245			250		255
Tyr Phe Phe Asn Asn Arg Glu Glu Gln Val Gly Thr Glu His Ala Lys						
	260		265			270
Lys Val Ile Asp Ile Ser Glu His Asn Gly Arg Ile Asn Asp Trp Lys						
	275		280			285
Lys Val Ile Asp Glu Asn Glu Val Asp Gly Val Ile Val Arg Leu Gly						
	290		295			300
Tyr Ser Gly Lys Glu Asp Lys Glu Leu Ala His Asn Ile Lys Glu Leu						
305		310		315		320
Asn Arg Leu Gly Ile Pro Tyr Gly Val Tyr Leu Tyr Thr Tyr Ala Glu						
	325		330			335
Asn Glu Thr Asp Ala Glu Ser Asp Ala Lys Gln Thr Ile Glu Leu Ile						
	340		345			350
Lys Lys Tyr Asn Met Asn Leu Ser Tyr Pro Ile Tyr Tyr Asp Val Glu						
	355		360			365
Asn Trp Glu Tyr Val Asn Lys Ser Lys Arg Ala Pro Ser Asp Thr Gly						
	370		375			380
Thr Trp Val Lys Ile Ile Asn Lys Tyr Met Asp Thr Met Lys Gln Ala						
385		390		395		400
Gly Tyr Gln Asn Val Tyr Val Tyr Ser Tyr Arg Ser Leu Leu Gln Thr						
	405		410			415
Arg Leu Lys His Pro Asp Ile Leu Lys His Val Asn Trp Val Ala Ala						
	420		425			430
Tyr Thr Asn Ala Leu Glu Trp Glu Asn Pro His Tyr Ser Gly Lys Lys						
	435		440			445
Gly Trp Gln Tyr Thr Ser Ser Glu Tyr Met Lys Gly Ile Gln Gly Arg						
	450		455			460
Val Asp Val Ser Val Trp Tyr						
465		470				

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1924 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

TACGTCTCAG CCTACTTTTG TAAGAGCAGA AGAATCTCCA CAAGTTGTCG AAAAATCTTC	60
ATTAGAGAAG AAATATGAGG AAGCAAAAGC AAAAGCTGAT ACTGCCAAGA AAGATTACGA	120

AACGGCTAAA AAGAAAGCAG AAGACGCTCA GAAAAAGTAT GAAGATGATC AGAAGAGAAC	180
TGAGGAGAAA GCTCGAAAAAG AAGCAGAAGC ATCTCAAAAA TTGAATGATG TGGCGCTTGT	240
TGTTCAAAAT GCATATAAAG AGTACCGAGA AGTTCAAAAT CAACGTAGTA AATATAAATC	300
TGACGCTGAA TATCAGAAAA AATTAACAGA GGTCTGACTCT AAAATAGAGA AGGCTAGGAA	360
AGAGCAACAG GACTTGCAAA ATAAATTTAA TGAAGTAAGA GCAGTTGTAG TTCCTGAACC	420
AAATGCGTTG GCTGAGACTA AGAAAAAGC AGAAGAAGCT AAAGCAGAAG AAAAAGTAGC	480
TAAGAGAAAA TATGATTATG CAACTCTAAA GGTAGCACTA GCGAAGAAAG AAGTAGAGGC	540
TAAGGAACTT GAAATTGAAA AACTTCAATA TGAAATTTCT ACTTTGGAAC AAGAAGTTGC	600
TACTGCTCAA CATCAAGTAG ATAATTTGAA AAAACTTCTT GCTGGTGCGG ATCCTGATGA	660
TGGCACAGAA GTTATAGAAG CTAAATTAAA AAAAGGAGAA GCTGAGCTAA ACGCTAAACA	720
AGCTGAGTTA GCAAAAAAAC AAACAGAACT TGAAAACTT CTTGACAGCC TTGATCCTGA	780
AGGTAAGACT CAGGATGAAT TAGATAAAGA AGCAGAAGAA GCTGAGTTGG ATAAAAAGC	840
TGATGAACTT CAAAATAAAG TTGCTGATTT AGAAAAAGAA ATTAGTAACC TTGAAATATT	900
ACTTGAGGG GCTGATNCTG AAGATGATAC TGCTGCTCTT CAAAATAAAT TAGCTACTAA	960
AAAAGCTGAA TTGGAAAAAA CTCAAAAAGA ATTAGATGCA GCTCTTAATG AGTTAGGCC	1020
TGATGGAGAT GAAGAAGAAA CTCCAGCGCC GGCTCCTCAA CCAGAGCAAC CAGCTCCTGC	1080
ACCAAAACCA GAGCAACCAG CTCCAGCTCC AAAACCAGAG CAACCAGCTC CTGCACCAAA	1140
ACCAGAGCAA CCAGCTCCAG CTCCAAACC AGAGCAACCA GCTCCAGCTC CAAAACCAGA	1200
GCAACCAGCT AAGCCGAGA AACCAGCTGA AGAGCCTACT CAACCAGAAA AACCAGCCAC	1260
TCCAAAAACA GGCTGGAAAC AAGAAAACGG TATGTGGTAT TTCTACAATA CTGATGGTTC	1320
AATGGCAATA GGTGCTCC AAAACAACGG TTCATGGTAC TACCTAAACG CTAACGGCGC	1380
TATGGCAACA GGTGGGTGA AAGATGGAGA TACCTGGTAC TATCTTGAAG CATCAGGTGC	1440
TATGAAAGCA AGCCAATGGT TCAAAGTATC AGATAAATGG TACTATGTCA ACAGCAATGG	1500
CGCTATGGCG ACAGGCTGGC TCCAATACAA TGGCTCATGG TACTACCTCA ACGCTAATGG	1560
TGATATGGCG ACAGGATGGC TCCAATACAA CGGTTTCATGG TATTACCTCA ACGCTAATGG	1620
TGATATGGCG ACAGGATGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG	1680
TGCTATGGCT ACAGGTTGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG	1740
TTCAATGGCA ACAGGTTGGG TGAAAGATGG AGATACCTGG TACTATCTTG AAGCATCAGG	1800
TGCTATGAAA GCAAGCCAAT GGTTCAAAGT ATCAGATAAA TGGTACTATG TCAATGGCTT	1860
AGGTGCCCTT GCAGTCAACA CAACTGTAGA TGGCTATAAA GTCAATGCCA ATGGTGAATG	1920
GGTT	1924

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

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Thr Ser Gln Pro Thr Phe Val Arg Ala Glu Glu Ser Pro Gln Val Val
1          5          10          15

Glu Lys Ser Ser Leu Glu Lys Lys Tyr Glu Glu Ala Lys Ala Lys Ala
20          25          30

Asp Thr Ala Lys Lys Asp Tyr Glu Thr Ala Lys Lys Lys Ala Glu Asp
35          40          45

Ala Gln Lys Lys Tyr Glu Asp Gln Lys Arg Thr Glu Glu Lys Ala
50          55          60

Arg Lys Glu Ala Glu Ala Ser Gln Lys Leu Asn Asp Val Ala Leu Val
65          70          75          80

Val Gln Asn Ala Tyr Lys Glu Tyr Arg Glu Val Gln Asn Gln Arg Ser
85          90          95

Lys Tyr Lys Ser Asp Ala Glu Tyr Gln Lys Lys Leu Thr Glu Val Asp
100         105         110

Ser Lys Ile Glu Lys Ala Arg Lys Glu Gln Gln Asp Leu Gln Asn Lys
115         120         125

Phe Asn Glu Val Arg Ala Val Val Val Pro Glu Pro Asn Ala Leu Ala
130         135         140

Glu Thr Lys Lys Lys Ala Glu Glu Ala Lys Ala Glu Glu Lys Val Ala
145         150         155         160

Lys Arg Lys Tyr Asp Tyr Ala Thr Leu Lys Val Ala Leu Ala Lys Lys
165         170         175

Glu Val Glu Ala Lys Glu Leu Glu Ile Glu Lys Leu Gln Tyr Glu Ile
180         185         190

Ser Thr Leu Glu Gln Glu Val Ala Thr Ala Gln His Gln Val Asp Asn
195         200         205

Leu Lys Lys Leu Leu Ala Gly Ala Asp Pro Asp Asp Gly Thr Glu Val
210         215         220

Ile Glu Ala Lys Leu Lys Lys Gly Glu Ala Glu Leu Asn Ala Lys Gln
225         230         235         240

Ala Glu Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys Leu Leu Asp Ser
245         250         255

Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu Leu Asp Lys Glu Ala Glu
260         265         270

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Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu Leu Gln Asn Lys Val Ala
 275 280 285
 Asp Leu Glu Lys Glu Ile Ser Asn Leu Glu Ile Leu Leu Gly Gly Ala
 290 295 300
 Asp Xaa Glu Asp Asp Thr Ala Ala Leu Gln Asn Lys Leu Ala Thr Lys
 305 310 315 320
 Lys Ala Glu Leu Glu Lys Thr Gln Lys Glu Leu Asp Ala Ala Leu Asn
 325 330 335
 Glu Leu Gly Pro Asp Gly Asp Glu Glu Glu Thr Pro Ala Pro Ala Pro
 340 345 350
 Gln Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro
 355 360 365
 Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro
 370 375 380
 Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu
 385 390 395 400
 Gln Pro Ala Lys Pro Glu Lys Pro Ala Glu Glu Pro Thr Gln Pro Glu
 405 410 415
 Lys Pro Ala Thr Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp
 420 425 430
 Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Ile Gly Trp Leu Gln Asn
 435 440 445
 Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly
 450 455 460
 Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala
 465 470 475 480
 Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val
 485 490 495
 Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser
 500 505 510
 Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Leu Gln
 515 520 525
 Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr
 530 535 540
 Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly
 545 550 555 560
 Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu
 565 570 575
 Asn Ala Asn Gly Ser Met Ala Thr Gly Trp Val Lys Asp Gly Asp Thr
 580 585 590
 Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser Gln Trp Phe
 595 600 605

Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala
 610 615 620

Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp
 625 630 635 640

Val

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

TGGACAGGTG AAAGGTCATG CTACATTTGT GAAATCCATG ACAACTGAAA TGTACCAAGA	60
ACAACAGAAC CATTCTCTCG CCTACAATCA ACGCTTGGNT TCGCAAAATC GCATTGTAGA	120
TCCTTTTTTG GCGGAGGGAT ATGAGGTCAA TTACCAAGTG TCTGACGACC CTGATGCAGT	180
CTATGGTTAC TTGTCTATTC CAAGTTTGGA AATCATGGAG CCGGTTTATT TGGGAGCAGA	240
TTATCATCAT TTAGGGATGG GCTTGGCTCA TGTGGATGGT ACACCGCTGC CTCTGGATGG	300
TACAGGGATT CGCTCAGTGA TTGCTGGGCA CCGTGCAGAG CCAAGCCATG TCTTTTTCCG	360
CCATTTGGAT CAGCTAAAAG TTGGAGATGC TCTTTATTAT GATAATGGCC AGGAAATTGT	420
AGAATATCAG ATGATGGACA CAGAGATTAT TTTACCGTCG GAATGGGAAA AATTAGAATC	480
GGTTAGCTCT AAAAATATCA TGACCTTGAT AACCTGCGAT CCGATTCCTA CCTTTAATAA	540
ACGCTTATTA GTGAATTTTG AACGAGTCGC TGTTTATCAA AAATCAGATC CACAAACAGC	600
TGCAGTTGCG AGGGTTGCTT TTACGAAAGA AGGACAATCT GTATCGCGTG TTGCAACCTC	660
TCAATGGTTG	670

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Gly Gln Val Lys Gly His Ala Thr Phe Val Lys Ser Met Thr Thr Glu	
1 5 10 15	
Met Tyr Gln Glu Gln Gln Asn His Ser Leu Ala Tyr Asn Gln Arg Leu	
20 25 30	

Xaa Ser Gln Asn Arg Ile Val Asp Pro Phe Leu Ala Glu Gly Tyr Glu
 35 40 45
 Val Asn Tyr Gln Val Ser Asp Asp Pro Asp Ala Val Tyr Gly Tyr Leu
 50 55 60
 Ser Ile Pro Ser Leu Glu Ile Met Glu Pro Val Tyr Leu Gly Ala Asp
 65 70 75 80
 Tyr His His Leu Gly Met Gly Leu Ala His Val Asp Gly Thr Pro Leu
 85 90 95
 Pro Leu Asp Gly Thr Gly Ile Arg Ser Val Ile Ala Gly His Arg Ala
 100 105 110
 Glu Pro Ser His Val Phe Phe Arg His Leu Asp Gln Leu Lys Val Gly
 115 120 125
 Asp Ala Leu Tyr Tyr Asp Asn Gly Gln Glu Ile Val Glu Tyr Gln Met
 130 135 140
 Met Asp Thr Glu Ile Ile Leu Pro Ser Glu Trp Glu Lys Leu Glu Ser
 145 150 155 160
 Val Ser Ser Lys Asn Ile Met Thr Leu Ile Thr Cys Asp Pro Ile Pro
 165 170 175
 Thr Phe Asn Lys Arg Leu Leu Val Asn Phe Glu Arg Val Ala Val Tyr
 180 185 190
 Gln Lys Ser Asp Pro Gln Thr Ala Ala Val Ala Arg Val Ala Phe Thr
 195 200 205
 Lys Glu Gly Gln Ser Val Ser Arg Val Ala Thr Ser Gln Trp Leu
 210 215 220

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 784 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

GATTGCTCCT TTGAAGGATT TGAGAGAAAC CATGTTGGAA ATTGCTTCTG GTGCTCAAAA 60
 TCTTCGTGCC AAGGAAGTTG GTGCCTATGA ACTGAGAGAA GTAACGCGCC AATTAAATGC 120
 TATGTTGGAT CAGATTGATC AGTTGATGGT AGCTATTCGT AGCCAGGAAG AAACGACCCG 180
 TCAGTACCAA CTTCAAGCCC TTTTCGAGCCA GATTAATCCA CATTTCCTCT ATAACACTTT 240
 GGACACCATC ATCTGGATGG CTGAATTTC A TGATAGTCAG CGAGTGGTGC AGGTGACCAA 300
 GTCCTTGGCA ACCTATTTCC GCTTGGCGCT CAATCAAGGC AAGGACTTGA TTTGTCTCTC ----- 360 -
 TGACGAAATC AATCATGTCC GCCAGTATCT CTTTATCCAG AAACAACGCT ATGGAGATAA 420

GCTGGAATAC GAAATTAATG AAAATGTTGC CTTTGATAAT TTAGTCTTAC CCAAGCTGGT 480
 CCTACAACCC CTTGTAGAAA ATGCTCTTTA CCATGGCATT AAGGAAAAGG AAGGTCAGGG 540
 CCATATTAAA CTTTCTGTCC AGAAACAGGA TTCGGGATTG GTCATCCGTA TTGAGGATGA 600
 TGGCGTTGGC TTCCAAGATG CTGGTGATAG TAGTCAAAGT CAACTCAAAC GTGGGGGAGT 660
 TGGTCTTCAA AATGTGCATC AACGGCTCAA ACTTCATTTT GGAGCCAATT ACCATATGAA 720
 GATTGATTCT AGACCCCAA AAGGGACGAA AGTTGAAATA TATATAAATA GAATAGAAAC 780
 TAGC 784

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ile Ala Pro Leu Lys Asp Leu Arg Glu Thr Met Leu Glu Ile Ala Ser
 1 5 10 15
 Gly Ala Gln Asn Leu Arg Ala Lys Glu Val Gly Ala Tyr Glu Leu Arg
 20 25 30
 Glu Val Thr Arg Gln Phe Asn Ala Met Leu Asp Gln Ile Asp Gln Leu
 35 40 45
 Met Val Ala Ile Arg Ser Gln Glu Glu Thr Thr Arg Gln Tyr Gln Leu
 50 55 60
 Gln Ala Leu Ser Ser Gln Ile Asn Pro His Phe Leu Tyr Asn Thr Leu
 65 70 75 80
 Asp Thr Ile Ile Trp Met Ala Glu Phe His Asp Ser Gln Arg Val Val
 85 90 95
 Gln Val Thr Lys Ser Leu Ala Thr Tyr Phe Arg Leu Ala Leu Asn Gln
 100 105 110
 Gly Lys Asp Leu Ile Cys Leu Ser Asp Glu Ile Asn His Val Arg Gln
 115 120 125
 Tyr Leu Phe Ile Gln Lys Gln Arg Tyr Gly Asp Lys Leu Glu Tyr Glu
 130 135 140
 Ile Asn Glu Asn Val Ala Phe Asp Asn Leu Val Leu Pro Lys Leu Val
 145 150 155 160
 Leu Gln Pro Leu Val Glu Asn Ala Leu Tyr His Gly Ile Lys Glu Lys
 165 170 175
 Glu Gly Gln Gly His Ile Lys Leu Ser Val Gln Lys Gln Asp Ser Gly
 180 185 190

Leu Val Ile Arg Ile Glu Asp Asp Gly Val Gly Phe Gln Asp Ala Gly
 195 200 205
 Asp Ser Ser Gln Ser Gln Leu Lys Arg Gly Gly Val Gly Leu Gln Asn
 210 215 220
 Val Asp Gln Arg Leu Lys Leu His Phe Gly Ala Asn Tyr His Met Lys
 225 230 235 240
 Ile Asp Ser Arg Pro Gln Lys Gly Thr Lys Val Glu Ile Tyr Ile Asn
 245 250 255
 Arg Ile Glu Thr Ser
 260

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGGCTC CATAATATCT ATAAGGGATT	60
TACCCACTAC AAATATTATA GAGCCGAAAA TTCACATCTA ATATATGCAG ACTACTTTGA	120
AATGAAATTA AAAAAATTAT TAAAGGATGA CACAAAAGTT TTTGAAAAAT CTACATTCAA	180
ATTTGTAGAA GGATATAAAA TATACCTGAC AGAATCTAAA GAATCTGGAA TTAAACAAAT	240
GGACAATGTC ATAAAATATT TTGAGTTTAT TGAATCTAAA AGTATTGCTT TATATTTTCA	300
AAAACGATTA AATGAGCTGA TAGAT	325

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Arg Ser Tyr Gly Thr Phe Phe Leu Gln Gln Asn Arg Leu His Asn Ile	1 5 10 15
Tyr Lys Gly Phe Thr His Tyr Lys Tyr Tyr Arg Ala Glu Asn Ser His	20 25 30
Leu Ile Tyr Ala Asp Tyr Phe Glu Met Lys Leu Lys Lys Leu Leu Lys	35 40 45
Asp Asp Thr Lys Val Phe Glu Lys Ser Thr Phe Lys Phe Val Glu Gly	50 55 60

Tyr Lys Ile Tyr Leu Thr Glu Ser Lys Glu Ser Gly Ile Lys Gln Met
65 70 75 80

Asp Asn Val Ile Lys Tyr Phe Glu Phe Ile Glu Ser Lys Ser Ile Ala
85 90 95

Leu Tyr Phe Gln Lys Arg Leu Asn Glu Leu Ile Asp
100 105

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAACGTTGAG AATTATTTGC GAATGTGTTT GGATAGCATT CAGAATCAGA CGTATCAAAA 60
 TTTTGAGTGT TTATTAATCA ATGATGGCTC TCCAGATCAT TCATCCAAA TATGTGAAGA 120
 ATTTGTAGAG AAAGATTCTC GTTCAAATA TTTTGAGAAA GCAAACGGCG GTCTTTCATC 180
 AGCTCGTAAC CTAGGTATTG AATGTTCTGGG GGGGGGCGTA CATTACTTTT GTAGACTC 238

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn Val Glu Asn Tyr Leu Arg Met Cys Leu Asp Ser Ile Gln Asn Gln
1 5 10 15
 Thr Tyr Gln Asn Phe Glu Cys Leu Leu Ile Asn Asp Gly Ser Pro Asp
20 25 30
 His Ser Ser Lys Ile Cys Glu Glu Phe Val Glu Lys Asp Ser Arg Phe
35 40 45
 Lys Tyr Phe Glu Lys Ala Asn Gly Gly Leu Ser Ser Ala Arg Asn Leu
50 55 60
 Gly Ile Glu Cys Ser Gly Gly Gly Val His Tyr Phe Cys Arg Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 742 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

CTACTATCAA	TCAAGTTCTT	CAGCCATTGA	GGCCACCATT	GAGGGCAACA	GCCAAACGAC	60
CATCAGCCAG	ACTAGCCACT	TTATTTCAGTC	TTATATCAA	AAACTAGAAA	CCACCTCGAC	120
TGGTTTGACC	CAGCAGACGG	ATGTTCTGGC	CTATGCTGAG	AATCCCAGTC	AAGACAAGGT	180
CGAGGGAATC	CGAGATTTGT	TTTTGACCAT	CTTGAAGTCA	GATAAGGACT	TGAAAACGT	240
TGTGCTGGTG	ACCAAATCTG	GTCAGGTCAT	TTCTACAGAT	GACAGTGTGC	AGATGAAAAC	300
TTCCTCTGAT	ATGATGGCTG	AGGATTGGTA	CCAAAAGGCC	ATTTCATCAGG	GAGCTATGCC	360
TGTTTTGACT	CCAGCTCGTA	AATCAGATAG	TCAGTGGGTC	ATTTCTGTCA	CTCAAGAACT	420
TGTTTGATGCA	AAGGGAGCCA	ATCTTGGTGT	GCTTCGTTTG	GATATTTCTT	ATGAAACTCT	480
GGAAGCCTAT	CTCAATCAAC	TCCAGTTGGG	GCAGCAGGGC	TTTGCCTTCA	TTATCAATGA	540
AAACCATGAA	TTTGTCTACC	ATCCTCAACA	CACAGTTTAT	AGTTCGTCTA	GCAAAATGGA	600
GGCTATGAAA	CCCTACATCG	ATACAGGTCA	GGGTTATACT	CCTGGTCACA	AATCCTACGT	660
CAGTCAAGAG	AAGATTGCAG	GAAGTGATTG	GACGGTGCTT	GGCGTGTCAT	CATTGGAAAA	720
GTTAGACCAG	GTTCGGAGTC	AG				742

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Tyr	Tyr	Gln	Ser	Ser	Ser	Ser	Ala	Ile	Glu	Ala	Thr	Ile	Glu	Gly	Asn	
1				5					10					15		
Ser	Gln	Thr	Thr	Ile	Ser	Gln	Thr	Ser	His	Phe	Ile	Gln	Ser	Tyr	Ile	
			20					25					30			
Lys	Lys	Leu	Glu	Thr	Thr	Ser	Thr	Gly	Leu	Thr	Gln	Gln	Thr	Asp	Val	
		35					40					45				
Leu	Ala	Tyr	Ala	Glu	Asn	Pro	Ser	Gln	Asp	Lys	Val	Glu	Gly	Ile	Arg	
	50					55					60					
Asp	Leu	Phe	Leu	Thr	Ile	Leu	Lys	Ser	Asp	Lys	Asp	Leu	Lys	Thr	Val	
65					70					75					80	
Val	Leu	Val	Thr	Lys	Ser	Gly	Gln	Val	Ile	Ser	Thr	Asp	Asp	Ser	Val	
				85					90					95		

Gln Met Lys Thr Ser Ser Asp Met Met Ala Glu Asp Trp Tyr Gln Lys
 100 105 110
 Ala Ile His Gln Gly Ala Met Pro Val Leu Thr Pro Ala Arg Lys Ser
 115 120 125
 Asp Ser Gln Trp Val Ile Ser Val Thr Gln Glu Leu Val Asp Ala Lys
 130 135 140
 Gly Ala Asn Leu Gly Val Leu Arg Leu Asp Ile Ser Tyr Glu Thr Leu
 145 150 155 160
 Glu Ala Tyr Leu Asn Gln Leu Gln Leu Gly Gln Gln Gly Phe Ala Phe
 165 170 175
 Ile Ile Asn Glu Asn His Glu Phe Val Tyr His Pro Gln His Thr Val
 180 185 190
 Tyr Ser Ser Ser Ser Lys Met Glu Ala Met Lys Pro Tyr Ile Asp Thr
 195 200 205
 Gly Gln Gly Tyr Thr Pro Gly His Lys Ser Tyr Val Ser Gln Glu Lys
 210 215 220
 Ile Ala Gly Thr Asp Trp Thr Val Leu Gly Val Ser Ser Leu Glu Lys
 225 230 235 240
 Leu Asp Gln Val Arg Ser Gln
 245

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GACAAAAACA TTAAACGTC CTGAGGTTTT ATCACCTGCA GGGACTTTAG AGAAGCTAAA	60
GGTAGCTGTT CAGTATGGAG CAGATGCTGT CTTTATCGGT GGTCAGGCCT ATGGTCTTCG	120
TAGCCGTGCG GGAAACTTTA CTTTCGAACA GATGGAAGAA GCGGTGCAGT TTGCGGCCAA	180
GTATGGTGCC AAGGTCTATG TAGCGGCTAA TATGGTTATG CACGAAGGAA ATGAAGCTGG	240
TGCTGGTGAG TGGTTCCGTA AACTGCGTGA TATCGGGATT GCAGCAGTTA TCGTATCTGA	300
CCCAGCCTTG ATTATGATTG CAGTGACTGA AGCACCAGGC CTTGAAATCC ACCTTTCTAC	360
CCAAGCCAGT GCCACTAACT ATGAAACCCT TGAGTTCTGG AAAGAGCTAG GCTTGACTCG	420
TGTCGTTTTA GCGCGTGAGG TTTCAATGGA AGAATTAGCT GAGATCCGCA AACGTACAGA	480
TGTTGAAATT GAAGCCTTTG TCCATGGAGC TATGTGTATT TCATACTCTG GACGTTGTAC	540
TCTTTCAAAC CACATGAGTA TGCCTGATGC CAACCGTGGT GGATGTTCTC AGTCATGCCG	600

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TTGGAAATAC GACCTTTACG ATATGCCATT TGGGAAAGAA CGTAAGAGTT TGCAGGGTGA      660
GATTCCAGAA GAATTTTCAA TGTCAGCCGT TGACATGTCT ATGATTGACC ANATTCCAGA      720
TATGATTGAA AATGGTGTGG ACAGTCTAAA AATCGAAGGA CGTATGNAGT CTATTCTACTA      780
NGTATCAACA GTAACCAACT GCTACAAGGC GGCTGTGGAT GCCTATCTTG AAAGTCCTGA      840
AAAGTTTGAA GCTATCAAAC AAGACTTGGT GGACGAGATG TGAAGGTTG CCCAACGTGA      900
ACTGGCTACA GGATTTTACT ATGGTACACC ATCTGAAAAT GAGCAGTTGT TTGGTGCTCG      960
TCGTAAAATC CCTGAGTACA AGTTTGTCGC TGAAGTGGTT TCTTATGATG ATGCGGCACA     1020
AACAGCAACT ATTCGTCAAC GAAACGTCAT TAACGAAGGG GACCAAGTTG AGTTTTATGG     1080
TCCAGGTTTC CGTCATTTTG AAACCTATAT TGAAGATTTG CATGATGCTA AAGGCAATAA     1140
AATCGACCGC GCTCCAAATC CAATGGAAct ATTGACTATT AAAGTCCCAC AACCTGTTCA     1200
ATCAGGAGAC ATGGTTCGAG CTCTTAAAGA GGGGCTTATC AATCTTTATA AGGAAGATGG     1260
AACCAGCGTC ACAGTTCGTG CT                                             1282

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(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

Thr Lys Thr Leu Lys Arg Pro Glu Val Leu Ser Pro Ala Gly Thr Leu
1           5           10           15
Glu Lys Leu Lys Val Ala Val Gln Tyr Gly Ala Asp Ala Val Phe Ile
20           25           30
Gly Gly Gln Ala Tyr Gly Leu Arg Ser Arg Ala Gly Asn Phe Thr Phe
35           40           45
Glu Gln Met Glu Glu Gly Val Gln Phe Ala Ala Lys Tyr Gly Ala Lys
50           55           60
Val Tyr Val Ala Ala Asn Met Val Met His Glu Gly Asn Glu Ala Gly
65           70           75           80
Ala Gly Glu Trp Phe Arg Lys Leu Arg Asp Ile Gly Ile Ala Ala Val
85           90           95
Ile Val Ser Asp Pro Ala Leu Ile Met Ile Ala Val Thr Glu Ala Pro
100          105          110
Gly Leu Glu Ile His Leu Ser Thr Gln Ala Ser Ala Thr Asn Tyr Glu
115          120          125
Thr Leu Glu Phe Trp Lys Glu Leu Gly Leu Thr Arg Val Val Leu Ala
130          135          140

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Arg Glu Val Ser Met Glu Glu Leu Ala Glu Ile Arg Lys Arg Thr Asp
 145 150 155 160
 Val Glu Ile Glu Ala Phe Val His Gly Ala Met Cys Ile Ser Tyr Ser
 165 170 175
 Gly Arg Cys Thr Leu Ser Asn His Met Ser Met Arg Asp Ala Asn Arg
 180 185 190
 Gly Gly Cys Ser Gln Ser Cys Arg Trp Lys Tyr Asp Leu Tyr Asp Met
 195 200 205
 Pro Phe Gly Lys Glu Arg Lys Ser Leu Gln Gly Glu Ile Pro Glu Glu
 210 215 220
 Phe Ser Met Ser Ala Val Asp Met Ser Met Ile Asp Xaa Ile Pro Asp
 225 230 235 240
 Met Ile Glu Asn Gly Val Asp Ser Leu Lys Ile Glu Gly Arg Met Xaa
 245 250 255
 Ser Ile His Xaa Val Ser Thr Val Thr Asn Cys Tyr Lys Ala Ala Val
 260 265 270
 Asp Ala Tyr Leu Glu Ser Pro Glu Lys Phe Glu Ala Ile Lys Gln Asp
 275 280 285
 Leu Val Asp Glu Met Trp Lys Val Ala Gln Arg Glu Leu Ala Thr Gly
 290 295 300
 Phe Tyr Tyr Gly Thr Pro Ser Glu Asn Glu Gln Leu Phe Gly Ala Arg
 305 310 315 320
 Arg Lys Ile Pro Glu Tyr Lys Phe Val Ala Glu Val Val Ser Tyr Asp
 325 330 335
 Asp Ala Ala Gln Thr Ala Thr Ile Arg Gln Arg Asn Val Ile Asn Glu
 340 345 350
 Gly Asp Gln Val Glu Phe Tyr Gly Pro Gly Phe Arg His Phe Glu Thr
 355 360 365
 Tyr Ile Glu Asp Leu His Asp Ala Lys Gly Asn Lys Ile Asp Arg Ala
 370 375 380
 Pro Asn Pro Met Glu Leu Leu Thr Ile Lys Val Pro Gln Pro Val Gln
 385 390 395 400
 Ser Gly Asp Met Val Arg Ala Leu Lys Glu Gly Leu Ile Asn Leu Tyr
 405 410 415
 Lys Glu Asp Gly Thr Ser Val Thr Val Arg Ala
 420 425

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 778 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TTCTCAGGAG ACCTTTAAAA ATATCACCAA TAGCTTCTCC ATGCAAATCA ATCGTCGCGT 60
 CAACCAAGGA ACGCCTCGTG GTGCTGGGAA TATCAAGGGT GAAGACATCA AAAAAATCAC 120
 CGAAAACAAG GCCATTGAGT CTTATGTCAA ACGTATCAAC GCTATCGGAG ATTTGACTGG 180
 ATATGACCTG ATTGAAACGC CAGAAACCAA GAAGAATCTC ACTGCTGATC GTGCCAAGCG 240
 TTTTGGAAGT AGCTTGATGA TTACAGGTGT CAATGACTCC TCTAAAGAAG ACAAGTTTGT 300
 CTCTGGTTCT TATAAACTAG TCGAAGGAGA GCACTTAACC AACGACGACA AGGATAAAAT 360
 CCTCTTGCAC AAGGACTTGG CAGCCAAACA CGGCTGGAAA GTAGGGGACA AGGTTAAACT 420
 GGACTCTAAT ATCTACGATG CAGATAATGA AAAAGGAGCC AAGGAAACAG TTGAAGTGAC 480
 AATCAAGGGA CTCTTTGATG GTCATAATAA GTCAGCAGTA ACCTACTCAC AAGAACTTTA 540
 CGAAAACACA GCTATTACAG ACATTCACAC TGCTGCAAAA CTTTATGGAT ACACAGAAGA 600
 CACAGCCATT TATGGGGACG CAACCTTCTT TGTAACAGCA GACAAGAACT TGGATGATGT 660
 TATGAAAGAG TTGAATGGCA TCAGTGGTAT CAACTGGAAG AGCTACACAC TCGTCAAGAG 720
 CTCCTCTAAC TACCCAGCTC TTGAGCAATC TATCTCTGGT ATGTACAAGA TGGCCAAC 778

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Gln Glu Thr Phe Lys Asn Ile Thr Asn Ser Phe Ser Met Gln Ile
 1 5 10 15
 Asn Arg Arg Val Asn Gln Gly Thr Pro Arg Gly Ala Gly Asn Ile Lys
 20 25 30
 Gly Glu Asp Ile Lys Lys Ile Thr Glu Asn Lys Ala Ile Glu Ser Tyr
 35 40 45
 Val Lys Arg Ile Asn Ala Ile Gly Asp Leu Thr Gly Tyr Asp Leu Ile
 50 55 60
 Glu Thr Pro Glu Thr Lys Lys Asn Leu Thr Ala Asp Arg Ala Lys Arg
 65 70 75 80
 Phe Gly Ser Ser Leu Met Ile Thr Gly Val Asn Asp Ser Ser Lys Glu
 85 90 95
 Asp Lys Phe Val Ser Gly Ser Tyr Lys Leu Val Glu Gly Glu His Leu
 100 105 110

Thr Asn Asp Asp Lys Asp Lys Ile Leu Leu His Lys Asp Leu Ala Ala
 115 120 125
 Lys His Gly Trp Lys Val Gly Asp Lys Val Lys Leu Asp Ser Asn Ile
 130 135 140
 Tyr Asp Ala Asp Asn Glu Lys Gly Ala Lys Glu Thr Val Glu Val Thr
 145 150 155 160
 Ile Lys Gly Leu Phe Asp Gly His Asn Lys Ser Ala Val Thr Tyr Ser
 165 170 175
 Gln Glu Leu Tyr Glu Asn Thr Ala Ile Thr Asp Ile His Thr Ala Ala
 180 185 190
 Lys Leu Tyr Gly Tyr Thr Glu Asp Thr Ala Ile Tyr Gly Asp Ala Thr
 195 200 205
 Phe Phe Val Thr Ala Asp Lys Asn Leu Asp Asp Val Met Lys Glu Leu
 210 215 220
 Asn Gly Ile Ser Gly Ile Asn Trp Lys Ser Tyr Thr Leu Val Lys Ser
 225 230 235 240
 Ser Ser Asn Tyr Pro Ala Leu Glu Gln Ser Ile Ser Gly Met Tyr Lys
 245 250 255
 Met Ala Asn

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AGTAAATGCG CAATCAAATT CATTAATATT AATAGATGAA CCTGAAATCT CACTTCATCC	60
GAGTGCAATC TATAAATTTA AAGAGTTTTT ACTTCAAGAG TGTTTAAATA AAAACATCA	120
AATTATTATC ACTACACATT CTACACAACT TATAAAGAT TTTCCTAGAG AAGCCGTGAA	180
ACTTTTAGTG AAAACGGAG AAAAGGTAGA TGTTATTGAA AATATTGATT ATCAGGATGC	240
ATTTTTTGAA TTAGGTGATG TGTATCATTC TAGGAAGATG ATTTATGTTG AAGATAGACT	300
AGCTAAATAT ATTCTAGAGT TTGTTATCAC TCATTCAGGT AGTGAGAATC TTAAACAGAA	360
TTTAGTAGTG AGATATATTC CTGGTGGAGC AAATCAAATA ATTTGTAATA ATATTTTAA	420
CTCATCGTAT TTAGATTCCG ATAACCATTA TTTTGGCTT GATGGAGATC AAAACACTAA	480
TGTTAGTGAA TCAAATAATT TAATGAACTA TCTTGAAAAT GGTGTTGTTA TATCAGATAA	540
AATTCCTGAA TCAGATAATA AAAATCTTGA TGATATTATA AAATTGATAA NGGGATGTCC	600

AATTAAATTT AATGTTTCAG GTAATAAAGG GCAAAAAAAT AATATTGAAT TAATTGCGAA 660

ACAAAGAAGC TTTATAGATT ATTGGGCTAA ATAC 694

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Val	Asn	Ala	Gln	Ser	Asn	Ser	Leu	Ile	Leu	Ile	Asp	Glu	Pro	Glu	Ile	1	5	10	15
Ser	Leu	His	Pro	Ser	Ala	Ile	Tyr	Lys	Phe	Lys	Glu	Phe	Leu	Leu	Gln	20	25	30	
Glu	Cys	Leu	Asn	Lys	Lys	His	Gln	Ile	Ile	Ile	Thr	Thr	His	Ser	Thr	35	40	45	
Gln	Leu	Ile	Lys	Asp	Phe	Pro	Arg	Glu	Ala	Val	Lys	Leu	Leu	Val	Lys	50	55	60	
Asn	Gly	Glu	Lys	Val	Asp	Val	Ile	Glu	Asn	Ile	Asp	Tyr	Gln	Asp	Ala	65	70	75	80
Phe	Phe	Glu	Leu	Gly	Asp	Val	Tyr	His	Ser	Arg	Lys	Met	Ile	Tyr	Val	85	90	95	
Glu	Asp	Arg	Leu	Ala	Lys	Tyr	Ile	Leu	Glu	Phe	Val	Ile	Thr	His	Ser	100	105	110	
Gly	Ser	Glu	Asn	Leu	Lys	Gln	Asn	Leu	Val	Val	Arg	Tyr	Ile	Pro	Gly	115	120	125	
Gly	Ala	Asn	Gln	Ile	Ile	Cys	Asn	Asn	Ile	Leu	Asn	Ser	Ser	Tyr	Leu	130	135	140	
Asp	Ser	Asp	Asn	His	Tyr	Phe	Trp	Leu	Asp	Gly	Asp	Gln	Asn	Thr	Asn	145	150	155	160
Val	Ser	Glu	Ser	Asn	Asn	Leu	Met	Asn	Tyr	Leu	Glu	Asn	Gly	Val	Val	165	170	175	
Ile	Ser	Asp	Lys	Ile	Pro	Glu	Ser	Asp	Asn	Lys	Asn	Leu	Asp	Asp	Ile	180	185	190	
Ile	Lys	Leu	Ile	Xaa	Gly	Cys	Pro	Ile	Lys	Phe	Asn	Val	Ser	Gly	Asn	195	200	205	
Lys	Gly	Gln	Lys	Asn	Asn	Ile	Glu	Leu	Ile	Ala	Lys	Gln	Arg	Ser	Phe	210	215	220	
Ile	Asp	Tyr	Trp	Ala	Lys	Tyr	225	230											

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```

TTACCGCGTT CATCAAGATG TCAAACAAGT CATGACCTAT CAACCCATGG TCGGAGAAAT      60
ATTGAGTGAA CAAGACACCC CAGCAAACGA AGAGCTTGTG CTTGCTATGA TTTATACTGA      120
AACAAAAGGA AAAGAAGGCG ATGTTATGCA GTCTAGTGAG TCTGCAAGTG GTTCCACCAA      180
CACCATCAAT GATAATGCCT CTAGCATTCG GCAAGGCATT CAAACTCTGA CAGGCAATCT      240
CTATCTGGCG CAGAAGAAGG GGGTAGATAT CTGGACAGCT GTTCAAGCCT ATAATTTTGG      300
ACCTGCCTAT ATCGATTTTA TCGCCCCAAA TGGCAAGGAA AATACCCTGG CTCTAGCCAA      360
ACAGTACTCT CGTGAGACTG TTGCCCCCTT GCTTGTAAT AGGACTGGAA AGACTTATAG      420
TTATATTAC CCCATTTCCA TTTTTCACGG TGCTGAACTC TATGTAAATG GAGGAAACTA      480
TTATTATTCT AGACAGGTAC GACTTAACCT TTACATCATC AAATGTTTCA CTCTCTTTTC      540
AACATCTGGC                                     550

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(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Tyr Arg Val His Gln Asp Val Lys Gln Val Met Thr Tyr Gln Pro Met
1           5           10           15
Val Arg Glu Ile Leu Ser Glu Gln Asp Thr Pro Ala Asn Glu Glu Leu
20          25          30
Val Leu Ala Met Ile Tyr Thr Glu Thr Lys Gly Lys Glu Gly Asp Val
35          40          45
Met Gln Ser Ser Glu Ser Ala Ser Gly Ser Thr Asn Thr Ile Asn Asp
50          55          60
Asn Ala Ser Ser Ile Arg Gln Gly Ile Gln Thr Leu Thr Gly Asn Leu
65          70          75          80
Tyr Leu Ala Gln Lys Lys Gly Val Asp Ile Trp Thr Ala Val Gln Ala
85          90          95
Tyr Asn Phe Gly Pro Ala Tyr Ile Asp Phe Ile Ala Gln Asn Gly Lys

```

284

100	105	110
Glu Asn Thr Leu Ala Leu Ala Lys Gln Tyr Ser Arg Glu Thr Val Ala		
115	120	125
Pro Leu Leu Gly Asn Arg Thr Gly Lys Thr Tyr Ser Tyr Ile His Pro		
130	135	140
Ile Ser Ile Phe His Gly Ala Glu Leu Tyr Val Asn Gly Gly Asn Tyr		
145	150	155
		160
Tyr Tyr Ser Arg Gln Val Arg Leu Asn Leu Tyr Ile Ile Lys Cys Phe		
165	170	175
Thr Leu Phe Ser Thr Ser Gly		
180		

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GTGGATGGGC TTAACTATC TTCGTATTCG CCGTGCGGCT AAAATTGTGG ACAATGAGGA	60
GTTTGAAGCC TTGATTCGTA CGGGTCAATT GATTGATTTG CGCGACCCAG CAGAATTCCA	120
CAGAAAACAT ATCCTTGGTG CACGCAATAT TCCTTCAAGT CAGTTGAAAA CTAGTCTTGC	180
AGCCCTTCGT AAAGATAAAC CTGTCCTTCT CTACGAAAAC CAACGTGCGC AACGAGTTAC	240
AAATGCAGCT CTTTACTTGA AAAAACAAGG TTTTCTGAG ATTTATATCC TTTCTTATGG	300
CTTGATTCT TGAAAGGGA AAGTGAAGAC TAGC	334

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Trp Met Gly Phe Asn Tyr Leu Arg Ile Arg Arg Ala Ala Lys Ile Val	
1	15
Asp Asn Glu Glu Phe Glu Ala Leu Ile Arg Thr Gly Gln Leu Ile Asp	
20	30
Leu Arg Asp Pro Ala Glu Phe His Arg Lys His Ile Leu Gly Ala Arg	
35	45

Asn Ile Pro Ser Ser Gln Leu Lys Thr Ser Leu Ala Ala Leu Arg Lys
 50 55 60
 Asp Lys Pro Val Leu Leu Tyr Glu Asn Gln Arg Ala Gln Arg Val Thr
 65 70 75 80
 Asn Ala Ala Leu Tyr Leu Lys Lys Gln Gly Phe Ser Glu Ile Tyr Ile
 85 90 95
 Leu Ser Tyr Gly Leu Asp Ser Trp Lys Gly Lys Val Lys Thr Ser
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ACTAAACCAG CATCGTTCGC AGGAAAATAA GGACAATAAT CGTGTCTCTT ATGTGGATGG	60
CAGCCAGTCA AGTCAGAAAA GTGAAACTT GACACCAGAC CAGGTTAGCC AGAAAGAAGG	120
AATTCAGGCT GAGCAAATTG TAATCAAAAT TACAGATCAG GGCTATGTAA CGTCACACGG	180
TGACCACTAT CATTACTATA ATGGGAAAGT TCCTTATGAT GCCCTCTTTA GTGAAGAACT	240
CTTGATGAAG GATCCAAACT ATCAACTTAA AGACGCTGAT ATTGTCAATG AAGTCAAGGG	300
TGTTTATATC ATCAAGGTCG ATGGAAAATA TTATGTCTAC CTGAAAGATG CAGCTCATGC	360
TGATAATGTT CGAACTAAAG ATGAAATCAA TCGTCAAAAA CAAGAACATG TCAAAGATAA	420
TGAGAAGGTT AACTCTAATG TTGCTGTAGC AAGGTCTCAG GGACGATATA CGACAAATGA	480
TGTTTATGTC TTTAATCCAG CTGATATTAT CGAAGATACG GGTAATGCTT ATATCGTTCC	540
TCATGGAGGT CACTATCACT ACATTCCCAA AAGCGATTTA TCTGCTAGTG AATTAGCAGC	600
AGCTAAAGCA CATCTGGCTG GAAAAAATAT GCAACCGAGT CAGTTAAGCT ATTCTTCAAC	660
AGCTAGTGAC AATAACACGC AATCTGTAGC AAAAGGATCA ACTAGCAAGC CAGCAAATAA	720
ATCTGAAAAT CTCCAGAGTC TTTTGAAGGA ACTCTATGAT TCACCTAGCG CCCAACGTTA	780
CAGTGAATCA GATGGCCTGG TCTTTGACCC TGCTAAGATT ATCAGTCGTA CACCAAATGG	840
AGTTGCGATT CCGCATGGCG ACCATTACCA CTTTATTCCT TACAGCAAGC TTTCTGCCTT	900
AGAAGAAAAG ATTGCCAGAA TGGTGCCTAT CAGTGGAAGT GGTTCTACAG TTTCTACAAA	960
TGCAAAACCT AATGAAGTAG TGTCTAGTCT AGGCAGTCTT TCAAGCAATC CTTCTTCTTT	1020
AACGACAAGT AAGGAGCTCT CTTAGCATC TGATGGTTAT ATTTTAAATC CAAAAGATAT	1080
CGTTGAAGAA ACGGCTACAG CTTATATTGT AAGACATGGT GATCATTTC ATTACATTCC	1140
AAAATCAAAT CAAATTGGGC AACCGACTCT TCCAAACAAT AGTCTAGCAA CACCTTCTCC	1200

ATCTCTTCCA ATCAATCCAG GAACTTCACA TGAGAAACAT GAAGAAGATG GATACGGATT 1260
 TGATGCTAAT CGTATTATCG CTGAAGATGA ATCAGGTTTT GTCATGAGTC ACGGAGACCA 1320
 CAATCATTAT TTCTTCAAGA AG 1342

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn Asn Arg Val Ser
 1 5 10 15
 Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu Asn Leu Thr Pro
 20 25 30
 Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu Gln Ile Val Ile
 35 40 45
 Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp His Tyr His
 50 55 60
 Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe Ser Glu Glu Leu
 65 70 75 80
 Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala Asp Ile Val Asn
 85 90 95
 Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly Lys Tyr Tyr Val
 100 105 110
 Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr Lys Asp Glu
 115 120 125
 Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn Glu Lys Val Asn
 130 135 140
 Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asn Asp
 145 150 155 160
 Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp Thr Gly Asn Ala
 165 170 175
 Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile Pro Lys Ser Asp
 180 185 190
 Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His Leu Ala Gly Lys
 195 200 205
 Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr Ala Ser Asp Asn
 210 215 220
 Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys

225		230		235		240
Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr Asp Ser Pro Ser						
	245			250		255
Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe Asp Pro Ala Lys						
	260		265		270	
Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro His Gly Asp His						
	275		280		285	
Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu Glu Glu Lys Ile						
	290		295		300	
Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr Val Ser Thr Asn						
305		310		315		320
Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser Leu Ser Ser Asn						
	325		330			335
Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser Ala Ser Asp Gly						
	340		345			350
Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr Ala Thr Ala Tyr						
	355		360		365	
Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro Lys Ser Asn Gln						
	370		375		380	
Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro						
385		390		395		400
Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp						
	405		410			415
Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly						
	420		425		430	
Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe Lys Lys						
	435		440		445	

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TGACTACCTT GAAATCCAC TTTACAGCTA TCTTGGTGGA TTCAACACTA AAGTTCTTCC	60
AACTCCAATG ATGAACATCA TCAACGGTGG TTCTCACTCT GACGCTCCAA TCGCTTTCCA	120
AGAGTTCATG ATCTTGCCAG TTGGTGCGCC AACATTTAAA GAAGCCCTTC GTTACGGTGC	180
TGAAATCTTC CACGCTCTTA AGAAAATCCT TAAATCACGT GGTGGGAAA CTGCCGTAGG	240
TGACGAAGGT GGATTCGCTC CTCGTTTCGA AGGAACTGAA GATGGTGTG AACTATCCT	300

TGCTGCGATT GAAGCTGCTG GATATGTACC AGGTAAAGAC GTATTTATCG GATTTGACTG 360
 TGCTTCATCA GAATTCTACG ATAAAGAACG TAAAGTTTAC GACTACACTA AATTTGAAGG 420
 TGAAGGTGCT GCTGTTGTA CATCTGCAGA ACAAATCGAC TACCTTGAAG AATTGGTTAA 480
 CAAATACCCA ATCATCACTA TTGAAGATGG TATGGATGAA AACGACTGGG ATGGTTGGAA 540
 AGCTCTTACT GAACGTCTTG GTAAGAAAGT ACAACTTGTT GGTGACGACT TCTTCGTAAC 600
 AAACACTGAC TACCTTGCAC GTGGTATCCA AGAAGGTGCT GCTAACTCAA TCCTTATCAA 660
 AGTTAACCAA ATCGGTACTC TTAAGTAAAC TTTTGAAGCT ATCGAAATGG CTAAAGAAGC 720
 TGGTTACACT GCTGTTGTAT CACACCGTTC AGGTGAAACT GAAGATTCAA CAATCGCTGA 780
 TATTGCAGTT GCAACTAACG CAGGACAAAT CAAGACTGGT TCACTTTCAC GTACAGACCG 840
 CATCGCTAAA TACAACCAAT TGCTTCGTAT CGAAGACCAA CTTGGTGAAG TAGCTGAATA 900
 TCGTGGATTG AAATCATTCT ACAACCTTAA AAAA 934

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asp Tyr Leu Glu Ile Pro Leu Tyr Ser Tyr Leu Gly Gly Phe Asn Thr
 1 5 10 15
 Lys Val Leu Pro Thr Pro Met Met Asn Ile Ile Asn Gly Gly Ser His
 20 25 30
 Ser Asp Ala Pro Ile Ala Phe Gln Glu Phe Met Ile Leu Pro Val Gly
 35 40 45
 Ala Pro Thr Phe Lys Glu Ala Leu Arg Tyr Gly Ala Glu Ile Phe His
 50 55 60
 Ala Leu Lys Lys Ile Leu Lys Ser Arg Gly Leu Glu Thr Ala Val Gly
 65 70 75 80
 Asp Glu Gly Gly Phe Ala Pro Arg Phe Glu Gly Thr Glu Asp Gly Val
 85 90 95
 Glu Thr Ile Leu Ala Ala Ile Glu Ala Ala Gly Tyr Val Pro Gly Lys
 100 105 110
 Asp Val Phe Ile Gly Phe Asp Cys Ala Ser Ser Glu Phe Tyr Asp Lys
 115 120 125
 Glu Arg Lys Val Tyr Asp Tyr Thr Lys Phe Glu Gly Glu Gly Ala Ala
 130 135 140
 Val Arg Thr Ser Ala Glu Gln Ile Asp Tyr Leu Glu Glu Leu Val Asn

145		150		155		160
Lys Tyr Pro Ile	Ile Thr Ile Glu Asp Gly Met Asp Glu Asn Asp Trp					
	165			170		175
Asp Gly Trp Lys	Ala Leu Thr Glu Arg Leu Gly Lys Lys Val Gln Leu					
	180		185			190
Val Gly Asp Asp	Phe Phe Val Thr Asn Thr Asp Tyr Leu Ala Arg Gly					
	195		200			205
Ile Gln Glu Gly	Ala Ala Asn Ser Ile Leu Ile Lys Val Asn Gln Ile					
	210		215			220
Gly Thr Leu Thr	Glu Thr Phe Glu Ala Ile Glu Met Ala Lys Glu Ala					
	225		230		235	240
Gly Tyr Thr Ala	Val Val Ser His Arg Ser Gly Glu Thr Glu Asp Ser					
	245		250			255
Thr Ile Ala Asp	Ile Ala Val Ala Thr Asn Ala Gly Gln Ile Lys Thr					
	260		265			270
Gly Ser Leu Ser	Arg Thr Asp Arg Ile Ala Lys Tyr Asn Gln Leu Leu					
	275		280			285
Arg Ile Glu Asp	Gln Leu Gly Glu Val Ala Glu Tyr Arg Gly Leu Lys					
	290		295			300
Ser Phe Tyr Asn	Leu Lys Lys					
	305		310			

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

TCGTATCTTT TTTTGGAGCA ATGTTGCGGT AGAAGGACAT TCCATGGATC CGACCCTAGC	60
GGATGGCGAA ATTCTCTTCG TTGTAAACA CCTTCCTATT GACCGTTTTG ATATCGTGGT	120
GGCCCATGAG GAAGATGGCA ATAAGGACAT CGTCAAGCGC GTGATTGGAA TGCCTGGCGA	180
CACCATTCGT TACGAAAATG ATAACTCTA CATCAATGAC AAAGAAACGG ACGAGCCTTA	240
TCTAGCAGAC TATATCAAAC GCTTCAAGGA TGACAACTC CAAAGCACTT ACTCAGGCAA	300
GGGCTTTGAA GGAAATAAAG GAACTTTCTT TAGAAGTATC GCTCAAAAAG CTCAAGCCTT	360
CACAGTTGAT GTCAACTACA ACACCAACTT TAGCTTTACT GTTCCAGAAG GAGAATACCT	420
TCTCCTCGGA GATGACCGCT TGGTTTCGAG CGACAGCCGC CACGTAGGTA CCTTCAAAGC	480
AAAAGATATC ACAGGGGAAG CTAAATTCCG CTTATGGCCA ATCACCCGTA TCGGAACATT	540
T	541

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Ile Phe Phe Trp Ser Asn Val Arg Val Glu Gly His Ser Met Asp
 1 5 10 15
 Pro Thr Leu Ala Asp Gly Glu Ile Leu Phe Val Val Lys His Leu Pro
 20 25 30
 Ile Asp Arg Phe Asp Ile Val Val Ala His Glu Glu Asp Gly Asn Lys
 35 40 45
 Asp Ile Val Lys Arg Val Ile Gly Met Pro Gly Asp Thr Ile Arg Tyr
 50 55 60
 Glu Asn Asp Lys Leu Tyr Ile Asn Asp Lys Glu Thr Asp Glu Pro Tyr
 65 70 75 80
 Leu Ala Asp Tyr Ile Lys Arg Phe Lys Asp Asp Lys Leu Gln Ser Thr
 85 90 95
 Tyr Ser Gly Lys Gly Phe Glu Gly Asn Lys Gly Thr Phe Phe Arg Ser
 100 105 110
 Ile Ala Gln Lys Ala Gln Ala Phe Thr Val Asp Val Asn Tyr Asn Thr
 115 120 125
 Asn Phe Ser Phe Thr Val Pro Glu Gly Glu Tyr Leu Leu Leu Gly Asp
 130 135 140
 Asp Arg Leu Val Ser Ser Asp Ser Arg His Val Gly Thr Phe Lys Ala
 145 150 155 160
 Lys Asp Ile Thr Gly Glu Ala Lys Phe Arg Leu Trp Pro Ile Thr Arg
 165 170 175
 Ile Gly Thr Phe
 180

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GGACTCTCTC AAAGATGTGA AAGCAAATGC TAGCGACAGC AAGCCTGCAC AGGACAAGAA

60

2025-10-10 14:44:40

GGATGCAAAA CAAGGAACGG AAGATAGTAA GGATTCAGAT AAGATGACTG AAACAAACTC 120
 AGTTCCGGCA GGAGTGATTG TGGTCAGTCT ACTTGCCCTC CTAGGCGTGA TTGCCTTCTG 180
 GCTGATTTCGC CGTAAGAAAG AGTCAGAAAT CCAGCAATTA AGCACGGAAT TGATCAAGGT 240
 TCTAGGACAG CTAGATGCAG AAAAAGCGGA TAAAAAAGTC CTTGCCAAAG CCCAAAACCT 300
 TCTCCAAGAA ACCCTTGATT TCGTGAAAGA AGAAAATGGC TCAGCAGAGA CAGAAACTAA 360
 ACTAGTAGAG GAGCTTAAAG CAATCCTTGA CAAACTCAAG 400

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Asp Ser Leu Lys Asp Val Lys Ala Asn Ala Ser Asp Ser Lys Pro Ala
 1 5 10 15
 Gln Asp Lys Lys Asp Ala Lys Gln Gly Thr Glu Asp Ser Lys Asp Ser
 20 25 30
 Asp Lys Met Thr Glu Thr Asn Ser Val Pro Ala Gly Val Ile Val Val
 35 40 45
 Ser Leu Leu Ala Leu Leu Gly Val Ile Ala Phe Trp Leu Ile Arg Arg
 50 55 60
 Lys Lys Glu Ser Glu Ile Gln Gln Leu Ser Thr Glu Leu Ile Lys Val
 65 70 75 80
 Leu Gly Gln Leu Asp Ala Glu Lys Ala Asp Lys Lys Val Leu Ala Lys
 85 90 95
 Ala Gln Asn Leu Leu Gln Glu Thr Leu Asp Phe Val Lys Glu Glu Asn
 100 105 110
 Gly Ser Ala Glu Thr Glu Thr Lys Leu Val Glu Glu Leu Lys Ala Ile
 115 120 125
 Leu Asp Lys Leu Lys
 130

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CAAGAAATCC TATCATCTCT TCCAGAAGCA AACAGAGACG AGGGGAATTC AGACTCAGTT 60
 GATTGAAGAA TCGCTTAGTC AGCAGACTAT AATCCAGTCC TTCAATGCTC AAACAGAATT 120
 TATCCAAAGA TTGCGTGAGG CTCATGACAA CTACTCAGGC TATTCTCAGT CAGCCATCTT 180
 TTATTCTTCA ACGGTCAATC CTTGACTCG CTTTGTAAT GCACTCATTT ATGCCCTTTT 240
 AGCTGGAGTA GGAGCTTATC GTATCATGAT GGGTTCAGCC TTGACCGTCG GTCGTTTAGT 300
 GACTTTTTTG AACTATGTTT AGCAATACAC CAAGCCCTTT AACGATATTT CTTCAGTGCT 360
 AGCTGAGTTG CAAAGTGCTC TGGCTTGCGT AGAGCGTATC TATGGAGTCT TAGATAGCCC 420
 TGAAGTGGCT GAAACAGGTA AGGAAGTCTT GACGACCAGT GACCAAGTTA AGGGAGCTAT 480
 TTCCTTTAAA CATGTCTCTT TTGGCTACCA TCCTGAAAAA ATTTTGATTA AGGACTTGTC 540
 TATCGATATT CCAGCTGGTA GTAAGGTAGC CATCGTTGGT CCGACAGGTG CTGGAAAATC 600
 AACTCTTATC AATCTCCTTA TGCCTTTTTT TCCCATTAGC TCGGGAGATA TCTTGCTGGA 660
 TGGGCAATCC ATTTATGATT ATACACGAGT ATCATTGAGA CAGCAGTTTG GTATGGTGCT 720
 TCAAGAAACC TGGCTCACAC AAGGGACCAT TCATGATAAT ATTGCCTTTG GCAATCCTGA 780
 AGCCAGTCGA GAGCAAGTAA TTGCTGCTGC CAAAGCAGCT AATGCAGACT TTTTCATCCA 840
 ACAGTTGCCA CAGGGATACG ATACCAAGTT GGAAAATGCT GGAGAATCTC TCTCTGTCGG 900
 CCAAGCTCAG CTCTTGACCA TAGCCCAGT CTTTCTGGCT ATTCCAAAGA TTCTTATCTT 960
 AGACGAGGCA ACTTCTTCCA TTGATACACG GACAGAAGTG CTGGTACAGG ATGCCTTTGC 1020
 AAAACTCATG AAGGGCCGCA CAAGTTTCAT CATTGCTCAC CGTTTGTCAA CCATTCAGGA 1080
 TGCGGATTTA ATTCTTGCTT TAGTAGATGG TGATATTGTT GAATATGGTA ACCATCAAGA 1140
 ACTCATGGAT AGAAAGGGTA AGTATTACCA AATGCAAAAA GCTGCGGCTT TTAGTTCTGA 1200
 A 1201

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Lys Ser Tyr His Leu Phe Gln Lys Gln Thr Glu Thr Arg Gly Ile
 1 5 10 15
 Gln Thr Gln Leu Ile Glu Glu Ser Leu Ser Gln Gln Thr Ile Ile Gln
 20 25 30

Asp Gly Asp Ile Val Glu Tyr Gly Asn His Gln Glu Leu Met Asp Arg
 370 375 380

Lys Gly Lys Tyr Tyr Gln Met Gln Lys Ala Ala Ala Phe Ser Ser Glu
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACGAAATGCA GGGCAGACAG ATGCCTCGCA AATTGAAAAG GCGGCAGTTA GCCAAGGAGG	60
AAAAGCAGTG AAAAAAACAG AAATTAGTAA AGACGCAGAC TTGCACGAAA TTTATCTAGC	120
TGGAGGTTGT TTCTGGGGAG TGGAGGAATA TTTCTCACGT GTTCCCGGGG TGACGGATGC	180
CGTTTCAGGC TATGCAAATG GTAGAGGAGA AACAACCAAG TACGAATTGA TTAACCAAAC	240
AGGTCATGCA GAAACCGTCC ATGTCACCTA TGATGCCAAG CAAATTTCTC TCAAGGAAAT	300
CCTGCTTCAC TATTTCCGCA TTATCAATCC AACCAGCAAA AATAAACAAG GAAATGATGT	360
GGGGACCCAG TACCGTACTG GTGTTTATTA CACAGATGAC AAGGATTTGG AAGTGATTAA	420
CCAAGTCTTT GATGAGGTGG CTAAGAAATA CGATCAACCT CTAGCAGTTG AAAAGGAAAA	480
CTTGAAGAAT TTTGTGGTGG CTGAGGATTA CCATCAAGAC TATCTCAAGA AAAATCCAAA	540
TGGCTACTGC CATATCAATG TTAATCAGGC GGCCTATCCT GTCATTGATG CCAGCAAATA	600
TCCAAAACCA AGTGATGAGG AATTGAAAAA GACCCTGTCA CCTGAGGAGT ATGCAGTTAC	660
CCAGGAAAAT CAAACAGAAC GAGCTTTCTC AAACCGTTAC TGGGATAAAT TTGAATCCGG	720
TATCTATGTG GATATAGCAA CTGGGGAACC TCTCTTTTCA TCAAAGACA AATTTGAGTC	780
TGGTTGTGGC TGGCCTAGTT TTACCCAACC CATCAGTCCA GATGTTGTCA CCTACAAGGA	840
AGATAAGTCC TACAATATGA CGCGTATGGA AGTGCGGAGC CGAGTAGGAG ATTCTCACCT	900
TGGGCATGTC TTTACGGATG GTCCACAGGA CAAGGGCGGC TTACGTTACT GTATCAATAG	960
CCTCTCTATC CGCTTTATTC CCAAAGACCA AATGGAAGAA AAAGGCTACG CTTATTTACT	1020
AGATTATGTT GAT	1033

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Leu Ser Ile Arg Phe Ile Pro Lys Asp Gln Met Glu Glu Lys Gly Tyr
 325 330 335

Ala Tyr Leu Leu Asp Tyr Val Asp
 340

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

TGTATAGTTT TTAGCGCTTG TTCTTCTAAT TCTGNTAAAA ATGAAGAAAA TACTTCTAAA	60
GAGCATGCGC CTGATAAAAT AGTTT TAGAT CATGCTTTCG GTCAAAC TAT ATTAGATAAA	120
AAACCTGAAA GAGTTGCAAC TATTGCTTGG GGAAATCATG ATGTAGCATT AGCTTTAGGA	180
ATAGTTCCTG TTGGATTTTC AAAAGCAAAT TACGGTGTA GTGCTGATAA AGGAGTTTTA	240
CCATGGACAG AAGAAAAAAT CAAAGAACTA AATGGTAAAG CTAACCTATT TGACGATTTG	300
GATGGACTTA ACTTTGAAGC AATATCAAAT TCTAAACCAG ATGTTATCTT AGCAGGTTAT	360
TCTGGTATAA CTAAAGAAGA TTATGACACT CTATCA	396

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Cys Ile Val Phe Ser Ala Cys Ser Ser Asn Ser Xaa Lys Asn Glu Glu	1 5 10 15
Asn Thr Ser Lys Glu His Ala Pro Asp Lys Ile Val Leu Asp His Ala	20 25 30
Phe Gly Gln Thr Ile Leu Asp Lys Lys Pro Glu Arg Val Ala Thr Ile	35 40 45
Ala Trp Gly Asn His Asp Val Ala Leu Ala Leu Gly Ile Val Pro Val	50 55 60
Gly Phe Ser Lys Ala Asn Tyr Gly Val Ser Ala Asp Lys Gly Val Leu	65 70 75 80
Pro Trp Thr Glu Glu Lys Ile Lys Glu Leu Asn Gly Lys Ala Asn Leu	85 90 95

Asp Thr Leu Ser
130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTGTGTCGAG	CATATTCTGA	AGCAAACCTA	TCAAAATATA	GAAATTATTT	TAGTTGATGA	60
CGGTTCTACG	GATAATTCTG	GGGAAATTTG	TGATGCTTTT	ATGATGCAAG	ATAATCGTGT	120
GCGAGTATTG	CATCAAGAAA	ATAAGGGGGG	GGCAGCACAA	GCTAAAAATA	TGGGGATTAG	180
TGTAGCTAAG	GGAGAGTACA	TCACGATTGT	TGATTTCAGAT	GATATCGTAA	AAGAAAATAT	240
GATTGAAACT	CTTTATCAGC	AAGTCCAAGA	AAAGGATGCA	GATGTTGTTA	TAGGGGAATTA	300
CTATAATTAT	GACGAAAGTG	ACGGGAATTT	TTATTTTTTAT	GTAACAGGGC	AAGATTTTTG	360
CGTCGAAGAA	TTAGCTATAC	AAGAAATTAT	GAACCGTCAA	GCAGGAGATT	GGAAATTCAA	420
TAGCTCGGCC	TTTATATTGC	CGACATTTAA	GTTGATTAAA	AAAGAATTAT	TCAATGAAGT	480
TCACTTTTCA	AATGGTCGCC	GCTTTGATGA	TGAAGCAACT	ATGCATCGCT	TTTATCTTTT	540
AGCCTCTAAA	ATCGTCTTTA	TAAACGATAA	TCTCTATCTG	TATAGAAGAC	G TTCAGGAAG	600
CATCATGAGA	ACGGAATTTG	ATCTTTCCTG	GGCAAGAGAT	ATTGTTGAAG	TGTTTTCTAA	660
GAAAATATCG	GATTGTGTCT	TGGCTGGTTT	GGATGTCTCC	GTTCTGCGTA	TTCGATTTGT	720
CAATCTTTTA	AAAGATTATA	AGCAAACTTT	AGAATACCAT	CAATTAACAG	ATACTGAGGA	780
ATATAAAGAT	ATTTGTTTCA	GATTAAAGTT	GTTTTTTGAT	GCAGAACAAA	GAAATGGTAA	840
AAGT						844

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Cys Val Glu His Ile Leu Lys Gln Thr Tyr Gln Asn Ile Glu Ile Ile
 1 5 10 15
 Leu Val Asp Asp Gly Ser Thr Asp Asn Ser Gly Glu Ile Cys Asp Ala
 20 25 30
 Phe Met Met Gln Asp Asn Arg Val Arg Val Leu His Gln Glu Asn Lys
 35 40 45
 Gly Gly Ala Ala Gln Ala Lys Asn Met Gly Ile Ser Val Ala Lys Gly
 50 55 60
 Glu Tyr Ile Thr Ile Val Asp Ser Asp Asp Ile Val Lys Glu Asn Met
 65 70 75 80
 Ile Glu Thr Leu Tyr Gln Gln Val Gln Glu Lys Asp Ala Asp Val Val
 85 90 95
 Ile Gly Asn Tyr Tyr Asn Tyr Asp Glu Ser Asp Gly Asn Phe Tyr Phe
 100 105 110
 Tyr Val Thr Gly Gln Asp Phe Cys Val Glu Glu Leu Ala Ile Gln Glu
 115 120 125
 Ile Met Asn Arg Gln Ala Gly Asp Trp Lys Phe Asn Ser Ser Ala Phe
 130 135 140
 Ile Leu Pro Thr Phe Lys Leu Ile Lys Lys Glu Leu Phe Asn Glu Val
 145 150 155 160
 His Phe Ser Asn Gly Arg Arg Phe Asp Asp Glu Ala Thr Met His Arg
 165 170 175
 Phe Tyr Leu Leu Ala Ser Lys Ile Val Phe Ile Asn Asp Asn Leu Tyr
 180 185 190
 Leu Tyr Arg Arg Arg Ser Gly Ser Ile Met Arg Thr Glu Phe Asp Leu
 195 200 205
 Ser Trp Ala Arg Asp Ile Val Glu Val Phe Ser Lys Lys Ile Ser Asp
 210 215 220
 Cys Val Leu Ala Gly Leu Asp Val Ser Val Leu Arg Ile Arg Phe Val
 225 230 235 240
 Asn Leu Leu Lys Asp Tyr Lys Gln Thr Leu Glu Tyr His Gln Leu Thr
 245 250 255
 Asp Thr Glu Glu Tyr Lys Asp Ile Cys Phe Arg Leu Lys Leu Phe Phe
 260 265 270
 Asp Ala Glu Gln Arg Asn Gly Lys Ser
 275 280

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GTGTTTGGAT AGCATTTCAGA ATCAGACGTA TCAAAATTTT GAGTGTTTAT TAATCAATGA 60
 TGGCTCTCCA GATCATTTCAT CCAAAATATG TGAAGAATTT GTAGAGAAAG ATTCTCGTTT 120
 CAAATATTTT GAGAAAGCAA ACGGCGGTCT TTCATCAGCT CGTAACCTAG GTATTGAATG 180
 TTCGGGGGGG GCGTACATTA CTTTGTAGA CTCTGATGAT TGGTTGGAAC ATGATGCTTT 240
 AGACCGATTA TATGGTGCTT TGAAAAAGGA AAACGCAGAT ATTAGTATCG GGC GTTATAA 300
 TTCTTATGAT GAAACACGCT ATGTGTATAT GACTTATGTT ACGGATCCAG ATGATTCTCT 360
 AGAAGTGATA GAAGGTAAAG CAATTATGGA TAGGGAAGGT GTCGAAGAAG TCAGAAATGG 420
 GAACTGGACT GTAGCTGTCT TGAAGTTATT CAAGAGAGAG TTACTACAAG ATTTACCATT 480
 TCCTATAGGA AAAATTGCAG AGGATACTTA CTGGACATGG AAGGTACTTC TAAGAGCTTC 540
 GAGGATAGTC TATTTGAATC GTTGTGTTTA CTGGTACCGT GTTGGTTTAT CTGATACTTT 600
 ATCGAATACA TGGAGTGAAA AGCGTATGTA TGATGAAATT GGGGCTAGGG AAGAAAAGAT 660
 AGCTATTTTA GCAAGTTCAG ACTATGACTT GACCAATCAT ATTTTGATTT ATAAAAATAG 720
 ATTACAAAGA GTGATAGCAA AATTAGAAGA ACAAATATG CAGTTCACAG AGATTACAG 780
 AAGAATGATG GAAAAATTGT CTTTACTTCC G 811

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Cys Leu Asp Ser Ile Gln Asn Gln Thr Tyr Gln Asn Phe Glu Cys Leu
 1 5 10 15
 Leu Ile Asn Asp Gly Ser Pro Asp His Ser Ser Lys Ile Cys Glu Glu
 20 25 30
 Phe Val Glu Lys Asp Ser Arg Phe Lys Tyr Phe Glu Lys Ala Asn Gly
 35 40 45
 Gly Leu Ser Ser Ala Arg Asn Leu Gly Ile Glu Cys Ser Gly Gly Ala
 50 55 60
 Tyr Ile Thr Phe Val Asp Ser Asp Asp Trp Leu Glu His Asp Ala Leu
 65 70 75 80
 Asp Arg Leu Tyr Gly Ala Leu Lys Lys Glu Asn Ala Asp Ile Ser Ile
 85 90 95

Gly Arg Tyr Asn Ser Tyr Asp Glu Thr Arg Tyr Val Tyr Met Thr Tyr
 100 105 110
 Val Thr Asp Pro Asp Asp Ser Leu Glu Val Ile Glu Gly Lys Ala Ile
 115 120 125
 Met Asp Arg Glu Gly Val Glu Glu Val Arg Asn Gly Asn Trp Thr Val
 130 135 140
 Ala Val Leu Lys Leu Phe Lys Arg Glu Leu Leu Gln Asp Leu Pro Phe
 145 150 155 160
 Pro Ile Gly Lys Ile Ala Glu Asp Thr Tyr Trp Thr Trp Lys Val Leu
 165 170 175
 Leu Arg Ala Ser Arg Ile Val Tyr Leu Asn Arg Cys Val Tyr Trp Tyr
 180 185 190
 Arg Val Gly Leu Ser Asp Thr Leu Ser Asn Thr Trp Ser Glu Lys Arg
 195 200 205
 Met Tyr Asp Glu Ile Gly Ala Arg Glu Glu Lys Ile Ala Ile Leu Ala
 210 215 220
 Ser Ser Asp Tyr Asp Leu Thr Asn His Ile Leu Ile Tyr Lys Asn Arg
 225 230 235 240
 Leu Gln Arg Val Ile Ala Lys Leu Glu Glu Gln Asn Met Gln Phe Thr
 245 250 255
 Glu Ile Tyr Arg Arg Met Met Glu Lys Leu Ser Leu Leu Pro
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGCCTAGAT AGTATTATTA CTCAAACATA TAAAAATATT GAGATTGTTG TCGTTAATGA	60
TGGTTCTACG GATGCTTCAG GTGAAATTTG TAAAGAATTT TCAGAAATGG ATCACCGAAT	120
TCTCTATATA GAACAAGAAA ATGCTGGTCT TTCTGCCGCA CGAAACACCG GTCTGAATAA	180
TATGTCCGGA AATTATGTGA CCTTTGTGGA CTCGGATGAT TGGATTGAGC AAGATTATGT	240
AGAAACTCTA TATAAAAAA TAGTAGAGTA TCAGGCTGAT ATTGCAGTTG GTAATTATTA	300
TTCTTTCAAC GAAAGTGAAG GAATGTTCTA CTTTCATATA TTGGGAGACT CCTATTATGA	360
GAAAGTATAT GATAATGTTT CTATCTTTGA GAACTGTAT GAACTCAAG AAATGAAGAG	420
TTTGTCTTTG ATATCTGCTT GGGGTAAACT CTATAAGGCA AGATTGTTTG AGCAGTTGCG	480
CTTTGACATA GGTAATTAG GAGAAGATGG TTACCTCAAT CAAAAGGTAT ATTTATTATC	540

AGAAAAGGTA ATTTATTTAA ATAAAAGTCT TTATGCTTAT CGGATTAGAA AAGGTAGTTT 600
 ATCAAGAGTT TGGACAGAAA AGTGGATGCA CGCTTTAGTT GATGCTATGT CTGAACGTAT 660
 TACGCTACTA GCTAATATGG GTTATCCTCT AGAGAAACAC TTGGCAGTTT ATCGTCAGAT 720
 GTTGGAAGTC AGTCTCGCCA ACGGTCAAGC TAGTGGTTTA TCTGACACAG CAACGTATAA 780
 AGAGTTTGAA ATGAAACAAA GGCTTTTAAA TCAGCTATCG AGACAAGAGG AAAGTGAAAA 840
 GAAAGCCATT GTCCTCGCAG CAAACTATGG CTATGTAGAC CAAGTTTTAA CGACAATCAA 900
 GTCTATTTGT TATCATAATC GTTCGATTCG TTTTATCTG ATTCATAGCG ATTTTCCAAA 960
 TGAATGGATT AAGCAATTAA ATAAGCGCTT AGAGAAGTTT GACTCAGAAA TTATTAATTG 1020
 TCGGGTAACT TCTGAGCAAA TTTCATGTTA TAAATCGGAT ATTAGTTACA CAGTCTTTTT 1080
 ACGCTATTTT ATAGCTGATT TCGTGCAAGA AGACAAGGCC CTCTACTTGG ACTGTGATCT 1140
 AGTTGTAACG AAAAATCTGG ATGACTTGTT TGCTACAGAC TTACAAGATT ATCCTTTGGC 1200
 TGCTGTTAGA GATTTTGGGG GCAGAGCTTA TTTTGGTCAA GAAATCTTTA ATGCCGGTGT 1260
 TCTCTTGGTA AACAATGCTT TTTGAAAAA AGAGAATATG ACCCAAAAAT TAATTGATGT 1320
 AACCAATGAA TGGCATGATA AGGTGGATCA GGCAGATCAG AGCATCTTGA ATATGCTTTT 1380
 TGAACATAAA TG GTTGAAT TGGACTTGA TTATAATCAT ATTGTCATTC ATAAACAGTT 1440
 TGCTGATTAT CAATTGCCTG AGGGTCAGGA TTATCCTGCT ATTATTCACT ATCTTTCTCA 1500
 TCGGAAACCG TGGAAAGATT TGGCGGCCCA AACCTATCGT GAAGTTTGGT GGTACTATCA 1560
 TGGGCTTGAA TGGACAGAAT TGGGACAAAA CCATCATTTA CATCCATTAC AAAGATCTCA 1620
 CATCTATCCA ATAAAGGAAC CTTTCACTTG TCTAATCTAT ACTGCCTCAG ACCATATTGA 1680
 ACAAATTGAG ACATTGGTTC AATCCTTGCC TGATATTCAG TTTAAGATAG CAGCTAGAGT 1740
 AATAGTTAGT GATCGATTGG CTCAGATGAC AATTTATCCA AACGTGACTA TATTTAACGG 1800
 AATTCATAT TTGGTAGATG TCGATAATGA ATTGGTAGAA ACCAGTCAAG TACTTTTAGA 1860
 TATTAATCAT GCGGAAAAGA CAGAAGAAAT TCTCGATCAA TTTGCTAATC TTGGCAAGCC 1920
 TATCTTATCC TTTGAAAATA CTAAAACCTA TGAAGTAGGT CAGGAGGCAT ATGCTGTTGA 1980
 CCAAGTTCAA GCAATGATTG AAAAATTGAG AGAAATAAGC AAA 2023

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

..(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Ser Lys

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

CATTCAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT GTTGATGATG GTGCAACAGA	60
TGAAAGTGGT CGCTTGTGTG ATTCAATCGC TGAACAAGAT GACAGGGTGT CAGTGCTTCA	120
TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG ATGAAGCAGG CTCACGGGGA	180
TTATCTGATT TTTATTGACT CAGATGATTA TATCCATCCA GAAATGATTC AGAGCTTATA	240
TGAGCAATTA GTTCAAGAAG ATGCGGATGT TTCGAGCTGT GGTGTCATGA ATGTCTATGC	300
TAATGATGAA AGCCACAGT CAGCCAATCA GGATGACTAT TTTGTCTGTG ATTCTCAAAC	360
ATTTCTAAAG GAATACCTCA TAGGTGAAAA AATACCTGGG ACGATTTGCA ATAAGCTAAT	420
CAAGAGACAG ATTGCAACTG CCCTATCCTT TCCTAAGGGG TTGATTTACG AAGATGCCTA	480
TTACCATTTT GATTTAATCA AGTTGGCCAA GAAGTATGTG GTTAATACTA AACCCATTATTA	540
TTACTATTTT CATAGAGGGG ATAGTATTAC GACCAAACCC TATGCAGAGA AGGATTTAGC	600
CTATATTGAT ATCTACCAA AGTTTTATAA TGAAGTTGTG AAAAATATC CTGACTTGAA	660
AGAGGTCGCT TTTTTCAGAT TGGCCTATGC CCACTTCTTT ATTCTGGATA AGATGTTGCT	720
AGATGATCAG TATAACAGT TTGAAGCCTA TTCTCAGATT CATCGTTTTT TAAAAGGCCA	780
TGCCTTTGCT ATTTCTAGGA ATCCAATTTT CCGTAAGGGG AGAAGAATTA GTGCTTTGGC	840
CCTATTCATA AATATTTCTT TATATCGATT CTTATTACTG AAAAATATTG AAAAATCTAA	900
AAAATTACAT	910

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ile	Gln	Lys	Gln	Thr	Tyr	Gln	Asn	Leu	Glu	Ile	Ile	Leu	Val	Asp	Asp
1				5					10					15	

Gly Ala Thr Asp Glu Ser Gly Arg Leu Cys Asp Ser Ile Ala Glu Gln
 20 25 30
 Asp Asp Arg Val Ser Val Leu His Lys Lys Asn Glu Gly Leu Ser Gln
 35 40 45
 Ala Arg Asn Asp Gly Met Lys Gln Ala His Gly Asp Tyr Leu Ile Phe
 50 55 60
 Ile Asp Ser Asp Asp Tyr Ile His Pro Glu Met Ile Gln Ser Leu Tyr
 65 70 75 80
 Glu Gln Leu Val Gln Glu Asp Ala Asp Val Ser Ser Cys Gly Val Met
 85 90 95
 Asn Val Tyr Ala Asn Asp Glu Ser Pro Gln Ser Ala Asn Gln Asp Asp
 100 105 110
 Tyr Phe Val Cys Asp Ser Gln Thr Phe Leu Lys Glu Tyr Leu Ile Gly
 115 120 125
 Glu Lys Ile Pro Gly Thr Ile Cys Asn Lys Leu Ile Lys Arg Gln Ile
 130 135 140
 Ala Thr Ala Leu Ser Phe Pro Lys Gly Leu Ile Tyr Glu Asp Ala Tyr
 145 150 155 160
 Tyr His Phe Asp Leu Ile Lys Leu Ala Lys Lys Tyr Val Val Asn Thr
 165 170 175
 Lys Pro Tyr Tyr Tyr Tyr Phe His Arg Gly Asp Ser Ile Thr Thr Lys
 180 185 190
 Pro Tyr Ala Glu Lys Asp Leu Ala Tyr Ile Asp Ile Tyr Gln Lys Phe
 195 200 205
 Tyr Asn Glu Val Val Lys Asn Tyr Pro Asp Leu Lys Glu Val Ala Phe
 210 215 220
 Phe Arg Leu Ala Tyr Ala His Phe Phe Ile Leu Asp Lys Met Leu Leu
 225 230 235 240
 Asp Asp Gln Tyr Lys Gln Phe Glu Ala Tyr Ser Gln Ile His Arg Phe
 245 250 255
 Leu Lys Gly His Ala Phe Ala Ile Ser Arg Asn Pro Ile Phe Arg Lys
 260 265 270
 Gly Arg Arg Ile Ser Ala Leu Ala Leu Phe Ile Asn Ile Ser Leu Tyr
 275 280 285
 Arg Phe Leu Leu Leu Lys Asn Ile Glu Lys Ser Lys Lys Leu His
 290 295 300

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1972 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

TAAGGCTGAT AATCGTGTTC AAATGAGAAC GACGATTAAT AATGAATCGC CATTGTTGCT	60
TTCTCCGTTG TATGGCAATG ATAATGGTAA CGGATTATGG TGGGGGAACA CATTGAAGGG	120
AGCATGGGAA GCTATTCTCG AAGATGTAA GCCATATGCA GCGATTGAAC TTCATCCTGC	180
AAAAGTCTGT AAACCAACAA GTTGTATTCC ACGAGATACG AAAGAATTGA GAGAATGGTA	240
TGTCAAGATG TTGGAGGAAG CTCAAAGTCT AAACATTCCA GTTTTCTTGG TTATTATGTC	300
GGCTGGAGAG CGTAATACAG TTCCTCCAGA GTGGTTAGAT GAACAATTCC AAAAGTATAG	360
TGTGTTAAAA GGTGTTTTAA ATATTGAGAA TTATTGGATT TACAATAACC AGTTAGCTCC	420
GCATAGTGCT AAATATTTGG AAGTTTGTGC CAAATATGGA GCGCATTTTA TCTGGCATGA	480
TCATGAAAAA TGGTTCTGGG AAACATTTAT GAATGATCCG ACATTCTTTG AAGCGAGTCA	540
AAAATATCAT AAAAATTTGG TGTTGGCAAC TAAAAATACG CCAATAAGAG ATGATGCGGG	600
TACAGATTCT ATCGTTAGTG GATTTTGGTT GAGTGGCTTA TGTGATAACT GGGGCTCATC	660
AACAGATACA TGGAAATGGT GGGAAAAACA TTATACAAAC ACATTTGAAA CTGGAAGAGC	720
TAGGGATATG AGATCCTATG CATCGGAACC AGAATCAATG ATTGCTATGG AAATGATGAA	780
TGTATATACT GGGGGAGGCA CAGTTTATAA TTTCGAATGT GCCGCGTATA CATTTATGAC	840
AAATGATGTA CCAACTCCAG CATTTACTAA AGGTATTATT CCTTTCTTTA GACATGCTAT	900
ACAAAATCCA GCTCCAAGTA AGGAAGAAGT TGTAAATAGA ACAAAGCTG TATTTTGGAA	960
TGGAGAAGGT AGGATTAGTT CATTAACGG ATTTTATCAA GGACTTTATT CGAATGATGA	1020
AACAATGCCT TTATATAATA ATGGGAGATA TCATATTCTT CCTGTAATAC ATGAGAAAAT	1080
TGATAAGGAA AAGATTTTCAT CTATATTCCC TAATGCAAAA ATTTTGACTA AAAATAGTGA	1140
GGAATTGTCT AGTAAAGTCA ACTATTTAAA CTCGCTTTAT CCAAACTTT ATGAAGGAGA	1200
TGGGTATGCT CAGCGTGTAG GTAATTCCTG GTATATTTAT AATAGTAATG CTAATATCAA	1260
TAAAAATCAG CAAGTAATGT TGCCTATGTA TACTAATAAT ACAAAGTCGT TATCGTTAGA	1320
TTTGACGCCA CATACTTACG CTGTTGTTAA AGAAAATCCA AATAATTTAC ATATTTTATT	1380
GAATAATTAC AGGACAGATA AGACAGCTAT GTGGGCATTA TCAGGAAATT TTGATGCATC	1440
AAAAAGTTGG AAGAAAGAAG AATTAGAGTT AGCGAACTGG ATAAGCAAAA ATTATTCCAT	1500
CAATCCTGTA GATAATGACT TTAGGACAAC AACACTTACA TTAAAGGGC AACTGGTCA	1560
TAAACCTCAG ATAAATATAA GTGGCGATAA AAATCATTAT ACTTATACAG AAAATTGGGA	1620
TGAGAATACC CATGTTTATA CCATTACGGT TAATCATAAT GGAATGGTAG AGATGTCTAT	1680
AAATACTGAG GGGACAGGTC CAGTCTCTTT CCCAACACCA GATAAATTTA ATGATGGTAA	1740
TTTGAATATA GCATATGCAA AACCAACAAC ACAAAGTTCT GTAGATTACA ATGGAGACCC	1800

TAATAGAGCT GTGGATGGTA ACAGAAATGG TAATTTTAAC TCTGGTTCGG TAACACACAC 1860
 TAGGGCAGAT AATCCCTCTT GGTGGGAAGT CGATTTGAAA AAAATGGATA AAGTTGGGCT 1920
 TGTAAAAATT TATAATCGCA CAGATGCTGA GACTCAACGT CTATCTAATT TT 1972

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Lys	Ala	Asp	Asn	Arg	Val	Gln	Met	Arg	Thr	Thr	Ile	Asn	Asn	Glu	Ser	1	5	10	15
Pro	Leu	Leu	Leu	Ser	Pro	Leu	Tyr	Gly	Asn	Asp	Asn	Gly	Asn	Gly	Leu	20	25	30	
Trp	Trp	Gly	Asn	Thr	Leu	Lys	Gly	Ala	Trp	Glu	Ala	Ile	Pro	Glu	Asp	35	40	45	
Val	Lys	Pro	Tyr	Ala	Ala	Ile	Glu	Leu	His	Pro	Ala	Lys	Val	Cys	Lys	50	55	60	
Pro	Thr	Ser	Cys	Ile	Pro	Arg	Asp	Thr	Lys	Glu	Leu	Arg	Glu	Trp	Tyr	65	70	75	80
Val	Lys	Met	Leu	Glu	Glu	Ala	Gln	Ser	Leu	Asn	Ile	Pro	Val	Phe	Leu	85	90	95	
Val	Ile	Met	Ser	Ala	Gly	Glu	Arg	Asn	Thr	Val	Pro	Pro	Glu	Trp	Leu	100	105	110	
Asp	Glu	Gln	Phe	Gln	Lys	Tyr	Ser	Val	Leu	Lys	Gly	Val	Leu	Asn	Ile	115	120	125	
Glu	Asn	Tyr	Trp	Ile	Tyr	Asn	Asn	Gln	Leu	Ala	Pro	His	Ser	Ala	Lys	130	135	140	
Tyr	Leu	Glu	Val	Cys	Ala	Lys	Tyr	Gly	Ala	His	Phe	Ile	Trp	His	Asp	145	150	155	160
His	Glu	Lys	Trp	Phe	Trp	Glu	Thr	Ile	Met	Asn	Asp	Pro	Thr	Phe	Phe	165	170	175	
Glu	Ala	Ser	Gln	Lys	Tyr	His	Lys	Asn	Leu	Val	Leu	Ala	Thr	Lys	Asn	180	185	190	
Thr	Pro	Ile	Arg	Asp	Asp	Ala	Gly	Thr	Asp	Ser	Ile	Val	Ser	Gly	Phe	195	200	205	
Trp	Leu	Ser	Gly	Leu	Cys	Asp	Asn	Trp	Gly	Ser	Ser	Thr	Asp	Thr	Trp	210	215	220	
Lys	Trp	Trp	Glu	Lys	His	Tyr	Thr	Asn	Thr	Phe	Glu	Thr	Gly	Arg	Ala				

225						230						235						240
Arg	Asp	Met	Arg	Ser 245	Tyr	Ala	Ser	Glu	Pro 250	Glu	Ser	Met	Ile	Ala 255	Met			
Glu	Met	Met	Asn 260	Val	Tyr	Thr	Gly	Gly 265	Gly	Thr	Val	Tyr	Asn 270	Phe	Glu			
Cys	Ala	Ala 275	Tyr	Thr	Phe	Met	Thr 280	Asn	Asp	Val	Pro	Thr 285	Pro	Ala	Phe			
Thr	Lys 290	Gly	Ile	Ile	Pro	Phe 295	Phe	Arg	His	Ala	Ile 300	Gln	Asn	Pro	Ala			
Pro 305	Ser	Lys	Glu	Glu 310	Val	Val	Asn	Arg	Thr	Lys 315	Ala	Val	Phe	Trp	Asn 320			
Gly	Glu	Gly	Arg	Ile 325	Ser	Ser	Leu	Asn	Gly 330	Phe	Tyr	Gln	Gly	Leu 335	Tyr			
Ser	Asn	Asp	Glu 340	Thr	Met	Pro	Leu	Tyr 345	Asn	Asn	Gly	Arg	Tyr 350	His	Ile			
Leu	Pro 355	Val	Ile	His	Glu	Lys	Ile 360	Asp	Lys	Glu	Lys 365	Ile	Ser	Ser	Ile			
Phe	Pro 370	Asn	Ala	Lys	Ile	Leu 375	Thr	Lys	Asn	Ser	Glu 380	Glu	Leu	Ser	Ser			
Lys 385	Val	Asn	Tyr	Leu 390	Asn	Ser	Leu	Tyr	Pro	Lys 395	Leu	Tyr	Glu	Gly	Asp 400			
Gly	Tyr	Ala	Gln 405	Arg	Val	Gly	Asn	Ser	Trp 410	Tyr	Ile	Tyr	Asn	Ser 415	Asn			
Ala	Asn	Ile	Asn 420	Lys	Asn	Gln	Gln	Val 425	Met	Leu	Pro	Met	Tyr 430	Thr	Asn			
Asn	Thr 435	Lys	Ser	Leu	Ser	Leu	Asp 440	Leu	Thr	Pro	His	Thr 445	Tyr	Ala	Val			
Val	Lys 450	Glu	Asn	Pro	Asn	Asn 455	Leu	His	Ile	Leu	Leu 460	Asn	Asn	Tyr	Arg			
Thr 465	Asp	Lys	Thr	Ala 470	Met	Trp	Ala	Leu	Ser	Gly 475	Asn	Phe	Asp	Ala	Ser 480			
Lys	Ser	Trp	Lys 485	Lys	Glu	Glu	Leu	Glu	Leu 490	Ala	Asn	Trp	Ile	Ser 495	Lys			
Asn	Tyr	Ser	Ile 500	Asn	Pro	Val	Asp 505	Asn	Asp	Phe	Arg	Thr	Thr 510	Thr	Leu			
Thr	Leu 515	Lys	Gly	His	Thr	Gly	His 520	Lys	Pro	Gln	Ile	Asn 525	Ile	Ser	Gly			
Asp	Lys 530	Asn	His	Tyr	Thr	Tyr 535	Thr	Glu	Asn	Trp	Asp 540	Glu	Asn	Thr	His			
Val 545	Tyr	Thr	Ile	Thr 550	Val	Asn	His	Asn	Gly	Met 555	Val	Glu	Met	Ser	Ile 560			
Asn	Thr	Glu	Gly	Thr	Gly	Pro	Val	Ser	Phe	Pro	Thr	Pro	Asp	Lys	Phe			

575

Val Lys Ile Tyr Asn Arg Thr Asp Ala Glu Thr Gln Arg Leu Ser Asn
645 650 655

Phe

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

CTGTGGCAAT	CAGTCAGCTG	CTTCCAAACA	GTCAGCTTCA	GGAACGATTG	AGGTGATTTC	60
ACGAGAAAAT	GGCTCTGGGA	CACGGGGTGC	CTTCACAGAA	ATCACAGGGA	TTCTCAAAAA	120
AGACGGTGAT	AAAAAAATTG	ACAACACTGC	CAAAACAGCT	GTGATTCAAA	ATAGTACAGA	180
AGGTGTTCTC	TCAGCAGTTC	AAGGGAATGC	TAATGCTATC	GGCTACATCT	CCTTGGGATC	240
TTTAACGAAA	TCTGTCAAGG	CTTTAGAGAT	TGATGGTGTC	AAGGCTAGTC	GAGACACAGT	300
TTTAGATGGT	GAATACCCTC	TTCAACGTCC	CTTCAACATT	GTTTGGTCTT	CTAATCTTTC	360
CAAGCTAGGT	CAAGATTTTA	TCAGCTTTAT	CCACTCCAAA	CAAGGTCAAC	AAGTGGTCAC	420
AGATAATAAA	TTTATTGAAG	CTAAAACCGA	AACCACGGAA	TATACAAGCC	AACACTTATC	480
AGGCAAGTTG	TCTGTTGTAG	GTTCCACTTC	AGTATCTTCT	TTAATGGAAA	AATTAGCAGA	540
AGCTTATAAA	AAAGAAAATC	CAGAAGTTAC	GATTGATATT	ACCTCTAATG	GGTCTTCAGC	600
AGGTATTACC	GCTGTTAAGG	AGAAAACCGC	TGATATTGGT	ATGGTTTCTA	GGGAATTAAC	660
TCCTGAAGAA	GGTAAGAGTC	TCACCCATGA	TGCTATTGCT	TTAGACGGTA	TTGCTGTTGT	720
GGTCAATAAT	GACAATAAGG	CAAGCCAAGT	CAGTATGGCT	GAACTTGCAG	ACGTTTTTAT	780
TGGCAAATTA	ACCACCTGGG	ACAAGATTAA	A			811

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Cys	Gly	Asn	Gln	Ser	Ala	Ala	Ser	Lys	Gln	Ser	Ala	Ser	Gly	Thr	Ile	1	5	10	15
Glu	Val	Ile	Ser	Arg	Glu	Asn	Gly	Ser	Gly	Thr	Arg	Gly	Ala	Phe	Thr	20	25	30	
Glu	Ile	Thr	Gly	Ile	Leu	Lys	Lys	Asp	Gly	Asp	Lys	Lys	Ile	Asp	Asn	35	40	45	
Thr	Ala	Lys	Thr	Ala	Val	Ile	Gln	Asn	Ser	Thr	Glu	Gly	Val	Leu	Ser	50	55	60	
Ala	Val	Gln	Gly	Asn	Ala	Asn	Ala	Ile	Gly	Tyr	Ile	Ser	Leu	Gly	Ser	65	70	75	80
Leu	Thr	Lys	Ser	Val	Lys	Ala	Leu	Glu	Ile	Asp	Gly	Val	Lys	Ala	Ser	85	90	95	
Arg	Asp	Thr	Val	Leu	Asp	Gly	Glu	Tyr	Pro	Leu	Gln	Arg	Pro	Phe	Asn	100	105	110	
Ile	Val	Trp	Ser	Ser	Asn	Leu	Ser	Lys	Leu	Gly	Gln	Asp	Phe	Ile	Ser	115	120	125	
Phe	Ile	His	Ser	Lys	Gln	Gly	Gln	Gln	Val	Val	Thr	Asp	Asn	Lys	Phe	130	135	140	
Ile	Glu	Ala	Lys	Thr	Glu	Thr	Thr	Glu	Tyr	Thr	Ser	Gln	His	Leu	Ser	145	150	155	160
Gly	Lys	Leu	Ser	Val	Val	Gly	Ser	Thr	Ser	Val	Ser	Ser	Leu	Met	Glu	165	170	175	
Lys	Leu	Ala	Glu	Ala	Tyr	Lys	Lys	Glu	Asn	Pro	Glu	Val	Thr	Ile	Asp	180	185	190	
Ile	Thr	Ser	Asn	Gly	Ser	Ser	Ala	Gly	Ile	Thr	Ala	Val	Lys	Glu	Lys	195	200	205	
Thr	Ala	Asp	Ile	Gly	Met	Val	Ser	Arg	Glu	Leu	Thr	Pro	Glu	Glu	Gly	210	215	220	
Lys	Ser	Leu	Thr	His	Asp	Ala	Ile	Ala	Leu	Asp	Gly	Ile	Ala	Val	Val	225	230	235	240
Val	Asn	Asn	Asp	Asn	Lys	Ala	Ser	Gln	Val	Ser	Met	Ala	Glu	Leu	Ala	245	250	255	
Asp	Val	Phe	Ser	Gly	Lys	Leu	Thr	Thr	Trp	Asp	Lys	Ile	Lys	260	265	270			

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

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TTGTCAACAA CAACATGCTA CTTCTGAGGG GACGAATCAA AGGCAAAGCA GTTCAGCGAA      60
AGTTCCATGG AAAGCTTCAT ACACCAACCT AAACAACCAG GTAAGTACAG AAGAGGTCAA      120
ATCTCTCTTA TCAGCTCACT TGGATCCAAA TAGTGTTGAT GCATTTTTTA ATCTCGTTAA      180
TGACTATAAT ACCATTGTCG GCTCAACTGG CTTATCAGGA GATTTCACTT CCTTTACTCA      240
CACCGAATAC GATGTTGAGA AAATCAGTCA TCTCTGGAAT CAAAAGAAGG GCGATTTTGT      300
TGGGACCAAC TGCCGTATCA ATAGTTATTG TCTTTTGAAA AATTCAGTCA CCATTCCAAA      360
GCTTGAAAAG AATGACCAGT TGCTTTTCCT AGATAATGAT GCGATTGATA AAGGAAAGGT      420
CTTTGATTCA CAAGATAAGG AAGAGTTTGA TATTCTATTT TCGAGAGTTC CAACTGAGTC      480
AACTACAGAT GTCAAGGTTC ACGCTGAAAA GATGGAAGCA TTCTTCTCAC AATTTC AATT      540
CAATGAAAAA GCTCGAATGC TGTCTGTAGT CTTGCACGAC AATTGATG GCGAGTATCT      600
GTTTGTAGGC CACGTTGGGG TCTTAGTACC TGCTGATGAC GGTTTCTTAT TTGTAGAGAA      660
ATTGACTTTC GAAGAGCCCT ACCAAGCGAT TAAATTTGCT AGTAAGGAAG ATTGCTACAA      720
GTATTTGGGC ACCAAGTATG CGGATTATAC AGGCGAGGGA CTGGCTAAGC CTTTATCAT      780
GGATAATGAT AAGTGGGTTA AACTT                                           805

```

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```

Cys Gln Gln Gln His Ala Thr Ser Glu Gly Thr Asn Gln Arg Gln Ser
1           5           10           15
Ser Ser Ala Lys Val Pro Trp Lys Ala Ser Tyr Thr Asn Leu Asn Asn
20           25           30
Gln Val Ser Thr Glu Glu Val Lys Ser Leu Leu Ser Ala His Leu Asp
35           40           45
Pro Asn Ser Val Asp Ala Phe Phe Asn Leu Val Asn Asp Tyr Asn Thr
50           55           60

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Ile	Val	Gly	Ser	Thr	Gly	Leu	Ser	Gly	Asp	Phe	Thr	Ser	Phe	Thr	His	65	70	75	80
Thr	Glu	Tyr	Asp	Val	Glu	Lys	Ile	Ser	His	Leu	Trp	Asn	Gln	Lys	Lys	85	90	95	
Gly	Asp	Phe	Val	Gly	Thr	Asn	Cys	Arg	Ile	Asn	Ser	Tyr	Cys	Leu	Leu	100	105	110	
Lys	Asn	Ser	Val	Thr	Ile	Pro	Lys	Leu	Glu	Lys	Asn	Asp	Gln	Leu	Leu	115	120	125	
Phe	Leu	Asp	Asn	Asp	Ala	Ile	Asp	Lys	Gly	Lys	Val	Phe	Asp	Ser	Gln	130	135	140	
Asp	Lys	Glu	Glu	Phe	Asp	Ile	Leu	Phe	Ser	Arg	Val	Pro	Thr	Glu	Ser	145	150	155	160
Thr	Thr	Asp	Val	Lys	Val	His	Ala	Glu	Lys	Met	Glu	Ala	Phe	Phe	Ser	165	170	175	
Gln	Phe	Gln	Phe	Asn	Glu	Lys	Ala	Arg	Met	Leu	Ser	Val	Val	Leu	His	180	185	190	
Asp	Asn	Leu	Asp	Gly	Glu	Tyr	Leu	Phe	Val	Gly	His	Val	Gly	Val	Leu	195	200	205	
Val	Pro	Ala	Asp	Asp	Gly	Phe	Leu	Phe	Val	Glu	Lys	Leu	Thr	Phe	Glu	210	215	220	
Glu	Pro	Tyr	Gln	Ala	Ile	Lys	Phe	Ala	Ser	Lys	Glu	Asp	Cys	Tyr	Lys	225	230	235	240
Tyr	Leu	Gly	Thr	Lys	Tyr	Ala	Asp	Tyr	Thr	Gly	Glu	Gly	Leu	Ala	Lys	245	250	255	
Pro	Phe	Ile	Met	Asp	Asn	Asp	Lys	Trp	Val	Lys	Leu					260	265		

(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TTGTTTCAGGC AAGTCCGTGA CTAGTGAACA CCAAACGAAA GATGAAATGA AGACGGAGCA	60
GACAGCTAGT AAAACAAGCG CAGCTAAAGG GAAAGAGGTG GCTGATTTTG AATTGATGGG	120
AGTAGATGGC AAGACCTACC GTTTATCTGA TTACAAGGGC AAGAAAGTCT ATCTCAAATT	180
CTGGGCTTCT TGGTGTTCCT TCTGTCTGGC TAGTCTTCCA GATACGGATG AGATTGCTAA	240
AGAAGCTGGT GATGACTATG TGGTCTTGAC AGTAGTGTC CAGGACATA AGGGAGAGCA	300
ATCTGAAGCG GACTTTAAGA ATTGGTATAA GGGATTGGAT TATAAAAATC TCCCAGTCCT	360

AGTTGACCCA TCAGGCAAAC TTTTGAAAC TTATGGTGTC CGTTCTTACC CAACCCAAGC 420
 CTTTATAGAC AAAGAAGGCA AGCTGGTCAA AACACATCCA GGATTCATGG AAAAAGATGC 480
 AATTTTGCAA ACTTTGAAGG AATTAGCC 508

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Cys	Ser	Gly	Lys	Ser	Val	Thr	Ser	Glu	His	Gln	Thr	Lys	Asp	Glu	Met	1	5	10	15
Lys	Thr	Glu	Gln	Thr	Ala	Ser	Lys	Thr	Ser	Ala	Ala	Lys	Gly	Lys	Glu	20	25	30	
Val	Ala	Asp	Phe	Glu	Leu	Met	Gly	Val	Asp	Gly	Lys	Thr	Tyr	Arg	Leu	35	40	45	
Ser	Asp	Tyr	Lys	Gly	Lys	Lys	Val	Tyr	Leu	Lys	Phe	Trp	Ala	Ser	Trp	50	55	60	
Cys	Ser	Ile	Cys	Leu	Ala	Ser	Leu	Pro	Asp	Thr	Asp	Glu	Ile	Ala	Lys	65	70	75	80
Glu	Ala	Gly	Asp	Asp	Tyr	Val	Val	Leu	Thr	Val	Val	Ser	Pro	Gly	His	85	90	95	
Lys	Gly	Glu	Gln	Ser	Glu	Ala	Asp	Phe	Lys	Asn	Trp	Tyr	Lys	Gly	Leu	100	105	110	
Asp	Tyr	Lys	Asn	Leu	Pro	Val	Leu	Val	Asp	Pro	Ser	Gly	Lys	Leu	Leu	115	120	125	
Glu	Thr	Tyr	Gly	Val	Arg	Ser	Tyr	Pro	Thr	Gln	Ala	Phe	Ile	Asp	Lys	130	135	140	
Glu	Gly	Lys	Leu	Val	Lys	Thr	His	Pro	Gly	Phe	Met	Glu	Lys	Asp	Ala	145	150	155	160
Ile	Leu	Gln	Thr	Leu	Lys	Glu	Leu	Ala	165										

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CTCGCAAATT GAAAAGGCGG CAGTTAGCCA AGGAGGAAAA GCAGTGAAAA AACAGAAAT 60
TAGTAAAGAC GCAGACTTGC ACGAAATTTA TCTAGCTGGA GGTGTTTTCT GGGGAGTGGA 120
GGAATATTTT TCACGTGTTT CCGGGGTGAC GGATGCCGTT TCAGGCTATG CAAATGGTAG 180
AGGAGAAACA ACCAAGTACG AATTGATTAA CCAAACAGGT CATGCAGAAA CCGTCCATGT 240
CACCTATGAT GCCAAGCAAA TTTCTCTCAA GGAAATCCTG CTTCACTATT TCCGCATTAT 300
CAATCCAACC AGCAAAAATA AACAAGGAAA TGATGTGGGG ACCCAGTACC GTACTGGTGT 360
TTATTACACA GATGACAAGG ATTTGGAAGT GATTAACCAA GTCTTTGATG AGGTGGCTAA 420
GAAATACGAT CAACCTCTAG CAGTTGAAAA GGAAACTTG AAGAATTTTG TGGTGGCTGA 480
GGATTACCAT CAAGACTATC TCAAGAAAAA TCCAAATGGC TACTGCCATA TCAATGTAA 540
TCAGGCGGCC TATCCTGTCA TTGATGCCAG CAAATATCCA AAACCAAGTG ATGAGGAATT 600
GAAAAAGACC CTGTCACCTG AGGAGTATGC AGTTACCCAG GAAAATCAAA CAGAACGAGC 660
TTTCTCAAAC CGTTACTGGG ATAAATTTGA ATCCGGTATC TATGTGGATA TAGCAACTGG 720
GGAACCTCTC TTTTCATCAA AAGACAAATT TGAGTCTGGT TGTGGCTGGC CTAGTTTTAC 780
CCAACCCATC AGTCCAGATG TTGTCACCTA CAAGGAAGAT AAGTCCTACA ATATGACGCG 840
TATGGAAGTG CGGAGCCGAG TAGGAGATTC TCACCTTGGG CATGTCTTTA CGGATGGTCC 900
ACAGGACAAG GGCGGCTTAC GTTACTGTAT CAATAGCCTC TCTATCCGCT TTATCCCAA 960
AGACCAAATG GAAGAAAAAG GTACGCTTAT TTAC 994

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ser Gln Ile Glu Lys Ala Ala Val Ser Gln Gly Gly Lys Ala Val Lys
1 5 10 15
Lys Thr Glu Ile Ser Lys Asp Ala Asp Leu His Glu Ile Tyr Leu Ala
20 25 30
Gly Gly Cys Phe Trp Gly Val Glu Glu Tyr Phe Ser Arg Val Pro Gly
35 40 45
Val Thr Asp Ala Val Ser Gly Tyr Ala Asn Gly Arg Gly Glu Thr Thr
50 55 60
Lys Tyr Glu Leu Ile Asn Gln Thr Gly His Ala Glu Thr Val His Val
65 70 75 80

(2) INFORMATION FOR SEQ ID NO: 213:

(A) LENGTH: 625 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTGTCAGTCA GGTTC TAATG GTTCTCAGTC TGCTGTGGAT GCTATCAAAC AAAAAGGGAA 60

ATTAGTTGTG GCAACCAGTC CTGACTATGC ACCCTTTGAA TTTCAATCAT TGTTTGATGG 120

AAAGAACCAG GTAGTCGGTG CAGACATCGA CATGGCTCAG GCTATCGCTG ATGAACTTGG 180
GGTTAAGTTG GAAATCTCAA GCATGAGTTT TGACAATGTT TTGACCAGTC TTCAAAGTGG 240
TAAGGCTGAC CTAGCAGTTG CAGGAATTAG TGCTACTGAC GAGAGAAAAG AAGTCTTTGA 300
TTTTTCAATC CCATACTATG AAAACAAGAT TAGTTTCTTG GTTCGTAAGG CTGATGTGGA 360
AAAATACAAG GATTTAAC TA GCCTAGAAAG TGCTAATATT GCAGCCCAA AAGGGACTGT 420
TCCAGAATCA ATGGTCAAGG AACAATTGCC AAAAGTTCAA TTAAGTTCCC TAACTAATAT 480
GGGTGAAGCA GTCAATGAAT TGCAGGCTGG AAAAATAGAT GCTGTTCATA TGGATGAGCC 540
TGTTGCACTT AGTTATGCTG CTAAAAACGC TGGCTTAGCT GTCGCAACTG TCAGCTTGAA 600
GATGAAGGAC GGCGACGCCA ATGCC 625

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Cys	Gln	Ser	Gly	Ser	Asn	Gly	Ser	Gln	Ser	Ala	Val	Asp	Ala	Ile	Lys	1	5	10	15
Gln	Lys	Gly	Lys	Leu	Val	Val	Ala	Thr	Ser	Pro	Asp	Tyr	Ala	Pro	Phe	20	25	30	
Glu	Phe	Gln	Ser	Leu	Val	Asp	Gly	Lys	Asn	Gln	Val	Val	Gly	Ala	Asp	35	40	45	
Ile	Asp	Met	Ala	Gln	Ala	Ile	Ala	Asp	Glu	Leu	Gly	Val	Lys	Leu	Glu	50	55	60	
Ile	Ser	Ser	Met	Ser	Phe	Asp	Asn	Val	Leu	Thr	Ser	Leu	Gln	Thr	Gly	65	70	75	80
Lys	Ala	Asp	Leu	Ala	Val	Ala	Gly	Ile	Ser	Ala	Thr	Asp	Glu	Arg	Lys	85	90	95	
Glu	Val	Phe	Asp	Phe	Ser	Ile	Pro	Tyr	Tyr	Glu	Asn	Lys	Ile	Ser	Phe	100	105	110	
Leu	Val	Arg	Lys	Ala	Asp	Val	Glu	Lys	Tyr	Lys	Asp	Leu	Thr	Ser	Leu	115	120	125	
Glu	Ser	Ala	Asn	Ile	Ala	Ala	Gln	Lys	Gly	Thr	Val	Pro	Glu	Ser	Met	130	135	140	
Val	Lys	Glu	Gln	Leu	Pro	Lys	Val	Gln	Leu	Thr	Ser	Leu	Thr	Asn	Met	145	150	155	160
Gly	Glu	Ala	Val	Asn	Glu	Leu	Gln	Ala	Gly	Lys	Ile	Asp	Ala	Val	His				

165

170

175

Met Asp Glu Pro Val Ala Leu Ser Tyr Ala Ala Lys Asn Ala Gly Leu
 180 185 190

Ala Val Ala Thr Val Ser Leu Lys Met Lys Asp Gly Asp Ala Asn Ala
 195 200 205

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

GGAAACTTCA CAGGATTTTA AAGAGAAGAA AACAGCAGTC ATTAAGGAAA AAGAAGTTGT	60
TAGTAAAAAT CCTGTGATAG ACAATAACAC TAGCAATGAA GAAGCAAAAA TCAAAGAAGA	120
AAATTCCAAT AAATCCCAAG GAGATTATAC GGACTCATTT GTGAATAAAA ACACAGAAAA	180
TCCCCAAAAA GAAGATAAAG TTGTCTATAT TGCTGAATTT AAAGATAAAG AATCTGGAGA	240
AAAAGCAATC AAGGAACTAT CCAGTCTTAA GAATACAAAA GTTTTATATA CTTATGATAG	300
AATTTTAAAC GGTAGTGCCA TAGAAACAAC TCCAGATAAC TTGGACAAAA TTAAACAAAT	360
AGAAGGTATT TCATCGGTTG AAAGGGCACA AAAAGTCCAA CCCATGATGA ATCATGCCAG	420
AAAGGAAATT GGAGTTGAGG AAGCTATTGA TTACCTAAAG TCTATCAATG CTCCGTTTGG	480
GAAAAATTTT GATGGTAGAG GTATGGTCAT TTCAAATATC GATACTGGAA CAGATTATAG	540
ACATAAGGCT ATGAGAATCG ATGATGATGC CAAAGCCTCA ATGAGATTTA AAAAAGAAGA	600
CTTAAAAGGC ACTGATAAAA ATTATTGGTT GAGTGATAAA ATCCCTCATG CGTTCAATTA	660
TTATAATGGT GGCAAAATCA CTGTAGAAAA ATATGATGAT GGAAGGGATT ATTTTGACCC	720
ACATGGGATG CATATTGCAG GGATTCTTGC TGGAAATGAT ACTGAACAAG ACATCAAAAA	780
CTTTAACGGC ATAGATGGAA TTGCACCTAA TGCACAAATT TTCTCTTACA AAATGTATTC	840
TGACGCAGGA TCTGGGTTTG CGGGTGATGA AACAATGTTT CATGCTATTG AAGATTCTAT	900
CAAACACAAC GTTGATGTTG TTTCGGTATC ATCTGGTTTT ACAGGAACAG GTCTTGTAGG	960
TGAGAAATAT TGGCAAGCTA TTCGGGCATT AAGAAAAGCA GGCATTCCAA TGGTTGTCGC	1020
TACGGGTAAC TATGCGACTT CTGCTTCAAG TTCTTCATGG GATTTAGTAG CAAATAATCA	1080
TCTGAAAATG ACCGACACTG GAAATGTAAC ACGAACTGCA GCACATGAAG ATGCGATAGC	1140
GGTCGCTTCT GCTAAAAATC AAACAGTTGA GTTTGATAAA GTTAACATAG GTGGAGAAAG	1200
TTTTAAATAC AGAAATATAG GGGCCTTTTT CGATAAGAGT AAAATCACAA CAAATGAAGA	1260
TGGAACAAAA GCTCCTAGTA AATTAAAATT TGTATATATA GGCAAGGGGC AAGACCAAGA	1320

TTTGATAGGT TTGGATCTTA GGGGCAAAAT TGCAGTAATG GATAGAATTT ATACAAAGGA 1380

TTTAAAAAAT GCTTTTAAAA AAGCTATGGA TAAGGGTGCA CGCGCCATTA TGGTTGTAAA 1440

TACTGTAAAT TACTACAATA GAGATAATTG GACAGAGCTT CCAGCTATGG GATATGAAGC 1500

GGATGAAGGT ACTAAAAGTC AAGTGT'TTTC AAT'TTCAGGA GATGATGGTG TAAAGCTATG 1560

GAACATGATT AATCCTGATA AAAAACTGA AGTCAAAAGA AATAATAAAG AAGATTTTAA 1620

AGATAAATTG GAGCAATACT ATCCAATTGA TATGGAAAGT TTTAATTCCA ACAAACCGAA 1680

TGTAGGTGAC GAAAAAGAGA TTGACTTTAA GTT'TGCACCT GACACAGACA AAGAACTCTA 1740

TAAAGAAGAT ATCATCGTTC CAGCAGGATC TACATCTTGG GGGCCAAGAA TAGATTTACT 1800

TTTAAAACCC GATGTTTCAG CACCTGGTAA AAATATTAAA TCCACGCTTA ATGTTATTAA 1860

TGGCAAATCA ACTTATGGCT ATATGTCAGG AACTAGTATG GCGACTCCAA TCGTGGCAGC 1920

TTCTACTGTT TTGATTAGAC CGAAATTAAA GGAAATGCTT GAAAGACCTG TATTGAAAAA 1980

TCTTAAGGGA GATGACAAAA TAGATCTTAC AAGTCTTACA AAAATTGCCC TACAAAATAC 2040

TGCGCGACCT ATGATGGATG CAACTTCTTG GAAAGAAAAA AGTCAATACT TTGCATCACC 2100

TAGACAACAG GGAGCAGGCC TAATTAATGT GGCCAATGCT TTGAGAAATG AAGTTGTAGC 2160

AAC'TTTCAAA AACACTGATT CTAAAGGTTT GGTAAACTCA TATGGTTCCA TTTCTCTTAA 2220

AGAAATAAAA GGTGATAAAA AATACTTTAC AATCAAGCTT CACAATACAT CAAACAGACC 2280

TTTGACTTTT AAAGTTTCAG CATCAGCGAT AACTACAGAT TCTCTAACTG ACAGATTAAA 2340

ACTTGATGAA ACATATAAAG ATGAAAAATC TCCAGATGGT AAGCAAATTG TTCCAGAAAT 2400

TCACCCAGAA AAAGTCAAAG GAGCAAATAT CACATTTGAG CATGATACTT TCACTATAGG 2460

CGCAAATTCT AGCTTTGATT TGAATGCGGT TATAAATGTT GGAGAGGCCA AAAACAAAAA 2520

TAAATTTGTA GAATCATTTA TTCATTTTGA GTCAGTGGAA GCGATGGAAG CTCTAAACTC 2580

CAGCGGGAAG AAAATAAACT TCCAACCTTC TTTGTCGATG CCTCTAATGG GATTTGCTGG 2640

GAATTGGAAC CACGAACCAA TCCTTGATAA ATGGGCTTGG GAAGAAGGGT CAAGATCAAA 2700

AACACTGGGA GGTATGATG ATGATGGTAA ACCGAAAATT CCAGGAACCT TAAATAAGGG 2760

AATTGGTGGA GAACATGGTA TAGATAAATT TAATCCAGCA GGAGTTATAC AAAATAGAAA 2820

AGATAAAAAT ACAACATCCC TGGATCAAAA TCCAGAATTA TTTGCTTTCA ATAACGAAGG 2880

GATCAACGCT CCATCATCAA GTGGTTCTAA GATTGCTAAC ATTTATCCTT TAGATTCAAA 2940

TGGAAATCCT CAAGATGCTC AACTTGAAAG AGGATTAACA CCTTCTCCAC TTGTATTAAAG 3000

AAGTGCAGAA GAAGGATTGA TT 3022

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1007 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Glu	Thr	Ser	Gln	Asp	Phe	Lys	Glu	Lys	Lys	Thr	Ala	Val	Ile	Lys	Glu	1	5	10	15
Lys	Glu	Val	Val	Ser	Lys	Asn	Pro	Val	Ile	Asp	Asn	Asn	Thr	Ser	Asn	20	25	30	
Glu	Glu	Ala	Lys	Ile	Lys	Glu	Glu	Asn	Ser	Asn	Lys	Ser	Gln	Gly	Asp	35	40	45	
Tyr	Thr	Asp	Ser	Phe	Val	Asn	Lys	Asn	Thr	Glu	Asn	Pro	Lys	Lys	Glu	50	55	60	
Asp	Lys	Val	Val	Tyr	Ile	Ala	Glu	Phe	Lys	Asp	Lys	Glu	Ser	Gly	Glu	65	70	75	80
Lys	Ala	Ile	Lys	Glu	Leu	Ser	Ser	Leu	Lys	Asn	Thr	Lys	Val	Leu	Tyr	85	90	95	
Thr	Tyr	Asp	Arg	Ile	Phe	Asn	Gly	Ser	Ala	Ile	Glu	Thr	Thr	Pro	Asp	100	105	110	
Asn	Leu	Asp	Lys	Ile	Lys	Gln	Ile	Glu	Gly	Ile	Ser	Ser	Val	Glu	Arg	115	120	125	
Ala	Gln	Lys	Val	Gln	Pro	Met	Met	Asn	His	Ala	Arg	Lys	Glu	Ile	Gly	130	135	140	
Val	Glu	Glu	Ala	Ile	Asp	Tyr	Leu	Lys	Ser	Ile	Asn	Ala	Pro	Phe	Gly	145	150	155	160
Lys	Asn	Phe	Asp	Gly	Arg	Gly	Met	Val	Ile	Ser	Asn	Ile	Asp	Thr	Gly	165	170	175	
Thr	Asp	Tyr	Arg	His	Lys	Ala	Met	Arg	Ile	Asp	Asp	Asp	Ala	Lys	Ala	180	185	190	
Ser	Met	Arg	Phe	Lys	Lys	Glu	Asp	Leu	Lys	Gly	Thr	Asp	Lys	Asn	Tyr	195	200	205	
Trp	Leu	Ser	Asp	Lys	Ile	Pro	His	Ala	Phe	Asn	Tyr	Tyr	Asn	Gly	Gly	210	215	220	
Lys	Ile	Thr	Val	Glu	Lys	Tyr	Asp	Asp	Gly	Arg	Asp	Tyr	Phe	Asp	Pro	225	230	235	240
His	Gly	Met	His	Ile	Ala	Gly	Ile	Leu	Ala	Gly	Asn	Asp	Thr	Glu	Gln	245	250	255	
Asp	Ile	Lys	Asn	Phe	Asn	Gly	Ile	Asp	Gly	Ile	Ala	Pro	Asn	Ala	Gln	260	265	270	
Ile	Phe	Ser	Tyr	Lys	Met	Tyr	Ser	Asp	Ala	Gly	Ser	Gly	Phe	Ala	Gly	275	280	285	

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Asp	Glu	Thr	Met	Phe	His	Ala	Ile	Glu	Asp	Ser	Ile	Lys	His	Asn	Val
290						295					300				
Asp	Val	Val	Ser	Val	Ser	Ser	Gly	Phe	Thr	Gly	Thr	Gly	Leu	Val	Gly
305					310					315					320
Glu	Lys	Tyr	Trp	Gln	Ala	Ile	Arg	Ala	Leu	Arg	Lys	Ala	Gly	Ile	Pro
				325					330					335	
Met	Val	Val	Ala	Thr	Gly	Asn	Tyr	Ala	Thr	Ser	Ala	Ser	Ser	Ser	Ser
			340					345					350		
Trp	Asp	Leu	Val	Ala	Asn	Asn	His	Leu	Lys	Met	Thr	Asp	Thr	Gly	Asn
		355					360					365			
Val	Thr	Arg	Thr	Ala	Ala	His	Glu	Asp	Ala	Ile	Ala	Val	Ala	Ser	Ala
	370					375					380				
Lys	Asn	Gln	Thr	Val	Glu	Phe	Asp	Lys	Val	Asn	Ile	Gly	Gly	Glu	Ser
385					390					395					400
Phe	Lys	Tyr	Arg	Asn	Ile	Gly	Ala	Phe	Phe	Asp	Lys	Ser	Lys	Ile	Thr
				405					410					415	
Thr	Asn	Glu	Asp	Gly	Thr	Lys	Ala	Pro	Ser	Lys	Leu	Lys	Phe	Val	Tyr
			420					425					430		
Ile	Gly	Lys	Gly	Gln	Asp	Gln	Asp	Leu	Ile	Gly	Leu	Asp	Leu	Arg	Gly
		435					440					445			
Lys	Ile	Ala	Val	Met	Asp	Arg	Ile	Tyr	Thr	Lys	Asp	Leu	Lys	Asn	Ala
		450				455					460				
Phe	Lys	Lys	Ala	Met	Asp	Lys	Gly	Ala	Arg	Ala	Ile	Met	Val	Val	Asn
465					470					475					480
Thr	Val	Asn	Tyr	Tyr	Asn	Arg	Asp	Asn	Trp	Thr	Glu	Leu	Pro	Ala	Met
				485					490					495	
Gly	Tyr	Glu	Ala	Asp	Glu	Gly	Thr	Lys	Ser	Gln	Val	Phe	Ser	Ile	Ser
			500					505					510		
Gly	Asp	Asp	Gly	Val	Lys	Leu	Trp	Asn	Met	Ile	Asn	Pro	Asp	Lys	Lys
		515					520					525			
Thr	Glu	Val	Lys	Arg	Asn	Asn	Lys	Glu	Asp	Phe	Lys	Asp	Lys	Leu	Glu
	530					535					540				
Gln	Tyr	Tyr	Pro	Ile	Asp	Met	Glu	Ser	Phe	Asn	Ser	Asn	Lys	Pro	Asn
545					550					555					560
Val	Gly	Asp	Glu	Lys	Glu	Ile	Asp	Phe	Lys	Phe	Ala	Pro	Asp	Thr	Asp
				565					570					575	
Lys	Glu	Leu	Tyr	Lys	Glu	Asp	Ile	Ile	Val	Pro	Ala	Gly	Ser	Thr	Ser
			580					585					590		
Trp	Gly	Pro	Arg	Ile	Asp	Leu	Leu	Leu	Lys	Pro	Asp	Val	Ser	Ala	Pro
		595					600					605			
Gly	Lys	Asn	Ile	Lys	Ser	Thr	Leu	Asn	Val	Ile	Asn	Gly	Lys	Ser	Thr
	610					615					620				

Tyr Gly Tyr Met Ser Gly Thr Ser Met Ala Thr Pro Ile Val Ala Ala
 625 630 635 640
 Ser Thr Val Leu Ile Arg Pro Lys Leu Lys Glu Met Leu Glu Arg Pro
 645 650 655
 Val Leu Lys Asn Leu Lys Gly Asp Asp Lys Ile Asp Leu Thr Ser Leu
 660 665 670
 Thr Lys Ile Ala Leu Gln Asn Thr Ala Arg Pro Met Met Asp Ala Thr
 675 680 685
 Ser Trp Lys Glu Lys Ser Gln Tyr Phe Ala Ser Pro Arg Gln Gln Gly
 690 695 700
 Ala Gly Leu Ile Asn Val Ala Asn Ala Leu Arg Asn Glu Val Val Ala
 705 710 715 720
 Thr Phe Lys Asn Thr Asp Ser Lys Gly Leu Val Asn Ser Tyr Gly Ser
 725 730 735
 Ile Ser Leu Lys Glu Ile Lys Gly Asp Lys Lys Tyr Phe Thr Ile Lys
 740 745 750
 Leu His Asn Thr Ser Asn Arg Pro Leu Thr Phe Lys Val Ser Ala Ser
 755 760 765
 Ala Ile Thr Thr Asp Ser Leu Thr Asp Arg Leu Lys Leu Asp Glu Thr
 770 775 780
 Tyr Lys Asp Glu Lys Ser Pro Asp Gly Lys Gln Ile Val Pro Glu Ile
 785 790 795 800
 His Pro Glu Lys Val Lys Gly Ala Asn Ile Thr Phe Glu His Asp Thr
 805 810 815
 Phe Thr Ile Gly Ala Asn Ser Ser Phe Asp Leu Asn Ala Val Ile Asn
 820 825 830
 Val Gly Glu Ala Lys Asn Lys Asn Lys Phe Val Glu Ser Phe Ile His
 835 840 845
 Phe Glu Ser Val Glu Ala Met Glu Ala Leu Asn Ser Ser Gly Lys Lys
 850 855 860
 Ile Asn Phe Gln Pro Ser Leu Ser Met Pro Leu Met Gly Phe Ala Gly
 865 870 875 880
 Asn Trp Asn His Glu Pro Ile Leu Asp Lys Trp Ala Trp Glu Glu Gly
 885 890 895
 Ser Arg Ser Lys Thr Leu Gly Gly Tyr Asp Asp Asp Gly Lys Pro Lys
 900 905 910
 Ile Pro Gly Thr Leu Asn Lys Gly Ile Gly Gly Glu His Gly Ile Asp
 915 920 925
 Lys Phe Asn Pro Ala Gly Val Ile Gln Asn Arg Lys Asp Lys Asn Thr
 930 935 940
 Thr Ser Leu Asp Gln Asn Pro Glu Leu Phe Ala Phe Asn Asn Glu Gly
 945 950 955 960

Thr Pro Ser Pro Leu Val Leu Arg Ser Ala Glu Glu Gly Leu Ile
995 1000 1005

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGTGGTCGAA	GTTGAGACTC	CTCAATCAAT	AACAAATCAG	GAGCAAGCTA	GGACAGAAAA	60
CCAAGTAGTA	GAGACAGAGG	AAGCTCCAAA	AGAAGAAGCA	CCTAAAACAG	AAGAAAGTCC	120
AAAGGAAGAA	CCAAAATCGG	AGGTAAAACC	TACTGACGAC	ACCCTTCCTA	AAGTAGAAGA	180
GGGGAAAGAA	GATTTCAGCAG	AACCAGCTCC	AGTTGAAGAA	GTAGGTGGAG	AAGTTGAGTC	240
AAAACCAGAG	GAAAAAGTAG	CAGTTAAGCC	AGAAAGTCAA	CCATCAGACA	AACCAGCTGA	300
GGAATCAAAA	GTTGAACAAG	CAGGTGAACC	AGTCGCGCCA	AGAGAAGACG	AAAAGGCACC	360
AGTCGAGCCA	GAAAAGCAAC	CAGAAGCTCC	TGAAGAAGAG	AAGGCTGTAG	AGGAAACACC	420
GAAACAAGAA	GAGTCAACTC	CAGATACCAA	GGCTGAAGAA	ACTGTAGAAC	CAAAAAGAGGA	480
GACTGTTAAT	CAATCTATTG	AACAACCCAA	AGTTGAAACG	CCTGCTGTAG	AAAAACAAAC	540
AGAACCAACA	GAGGAACCAA	AAGTTGAACA	AGCAGGTGAA	CCAGTCGCGC	CAAGAGAAGA	600
CGAACAGGCA	CCAACGGCAC	CAGTTGAGCC	AGAAAAGCAA	CCAGAAGTTC	CTGAAGAAGA	660
GAAGGCTGTA	GAGGAAACAC	CGAAACCAGA	AGATAAAATA	AAGGGTATTG	GTACTAAAGA	720
ACCAGTTGAT	AAAAGTGAGT	TAAATAATCA	AATTGATAAA	GCTAGTTCAG	TTTCTCCTAC	780
TGATTATTCT	ACAGCAAGTT	ACAATGCTCT	TGGACCTGTT	TTAGAAACTG	CAAAGGTGT	840
CTATGCTTCA	GAGCCTGTAA	AACAGCCTGA	GGTAAATAGC	GAGACAAATA	AACTTAAAC	900
GGCTATTGAC	GCTCTAAACG	TTGATAAAAC	TGAATTAAAC	AATACGATTG	CAGATGCAAA	960
AACAAAGGTA	AAAGAACATT	ACAGTGATAG	AAGTTGGCAA	AACCTCCAAA	CTGAAGTTAC	1020
AAAGGCTGAA	AAAGTTGCAG	CTAATACAGA	TGCTAAACAA	AGTGAAGTTA	ACGAAGCTGT	1080
TGAAAAATTA	ACTGCAACTA	TTGAAAAATT	GGTTGAATTA	TCTGAAAAGC	CAATATTAAC	1140
ATTGACTAGT	ACCGATAAGA	AAATATTGGA	ACGTGAAGCT	GTTGCTAAGT	ATACTCTAGA	1200
AAATCAAAAC	AAAACAAAAA	TCAAATCAAT	CACAGCTGAA	TTGAAAAAAG	GAGAAGAAGT	1260

(2) INFORMATION FOR SEQ ID NO:218:

(A) LENGTH: 565 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Val 1	Val	Glu	Val	Glu	Thr	Pro	Gln	Ser	Ile	Thr	Asn	Gln	Glu	Gln	Ala
				5					10					15	
Arg	Thr	Glu	Asn	Gln	Val	Val	Glu	Thr	Glu	Glu	Ala	Pro	Lys	Glu	Glu
			20					25					30		
Ala	Pro	Lys	Thr	Glu	Glu	Ser	Pro	Lys	Glu	Glu	Pro	Lys	Ser	Glu	Val
		35					40					45			
Lys	Pro	Thr	Asp	Asp	Thr	Leu	Pro	Lys	Val	Glu	Glu	Gly	Lys	Glu	Asp
	50					55					60				
Ser	Ala	Glu	Pro	Ala	Pro	Val	Glu	Glu	Val	Gly	Gly	Glu	Val	Glu	Ser
65					70					75					80
Lys	Pro	Glu	Glu	Lys	Val	Ala	Val	Lys	Pro	Glu	Ser	Gln	Pro	Ser	Asp
				85					90					95	
Lys	Pro	Ala	Glu	Glu	Ser	Lys	Val	Glu	Gln	Ala	Gly	Glu	Pro	Val	Ala
			100					105					110		
Pro	Arg	Glu	Asp	Glu	Lys	Ala	Pro	Val	Glu	Pro	Glu	Lys	Gln	Pro	Glu
		115					120					125			
Ala	Pro	Glu	Glu	Glu	Lys	Ala	Val	Glu	Glu	Thr	Pro	Lys	Gln	Glu	Glu
	130					135					140				
Ser	Thr	Pro	Asp	Thr	Lys	Ala	Glu	Glu	Thr	Val	Glu	Pro	Lys	Glu	Glu
145					150					155					160
Thr	Val	Asn	Gln	Ser	Ile	Glu	Gln	Pro	Lys	Val	Glu	Thr	Pro	Ala	Val
				165					170					175	
Glu	Lys	Gln	Thr	Glu	Pro	Thr	Glu	Glu	Pro	Lys	Val	Glu	Gln	Ala	Gly

Year	Total population		Male		Female		Total population	Male		Female		Total population	Male		Female			
	Population	%	Population	%	Population	%		Population	%	Population	%		Population	%	Population	%		
1950	1,000,000	100	500,000	50	500,000	50	1,000,000	100	500,000	50	500,000	50	1,000,000	100	500,000	50	500,000	50
1955	1,050,000	105	525,000	50	525,000	50	1,050,000	105	525,000	50	525,000	50	1,050,000	105	525,000	50	525,000	50
1960	1,100,000	110	550,000	50	550,000	50	1,100,000	110	550,000	50	550,000	50	1,100,000	110	550,000	50	550,000	50
1965	1,150,000	115	575,000	50	575,000	50	1,150,000	115	575,000	50	575,000	50	1,150,000	115	575,000	50	575,000	50
1970	1,200,000	120	600,000	50	600,000	50	1,200,000	120	600,000	50	600,000	50	1,200,000	120	600,000	50	600,000	50
1975	1,250,000	125	625,000	50	625,000	50	1,250,000	125	625,000	50	625,000	50	1,250,000	125	625,000	50	625,000	50
1980	1,300,000	130	650,000	50	650,000	50	1,300,000	130	650,000	50	650,000	50	1,300,000	130	650,000	50	650,000	50
1985	1,350,000	135	675,000	50	675,000	50	1,350,000	135	675,000	50	675,000	50	1,350,000	135	675,000	50	675,000	50
1990	1,400,000	140	700,000	50	700,000	50	1,400,000	140	700,000	50	700,000	50	1,400,000	140	700,000	50	700,000	50
1995	1,450,000	145	725,000	50	725,000	50	1,450,000	145	725,000	50	725,000	50	1,450,000	145	725,000	50	725,000	50
2000	1,500,000	150	750,000	50	750,000	50	1,500,000	150	750,000	50	750,000	50	1,500,000	150	750,000	50	750,000	50
2005	1,550,000	155	775,000	50	775,000	50	1,550,000	155	775,000	50	775,000	50	1,550,000	155	775,000	50	775,000	50
2010	1,600,000	160	800,000	50	800,000	50	1,600,000	160	800,000	50	800,000	50	1,600,000	160	800,000	50	800,000	50
2015	1,650,000	165	825,000	50	825,000	50	1,650,000	165	825,000	50	825,000	50	1,650,000	165	825,000	50	825,000	50
2020	1,700,000	170	850,000	50	850,000	50	1,700,000	170	850,000	50	850,000	50	1,700,000	170	850,000	50	850,000	50
2025	1,750,000	175	875,000	50	875,000	50	1,750,000	175	875,000	50	875,000	50	1,750,000	175	875,000	50	875,000	50
2030	1,800,000	180	900,000	50	900,000	50	1,800,000	180	900,000	50	900,000	50	1,800,000	180	900,000	50	900,000	50
2035	1,850,000	185	925,000	50	925,000	50	1,850,000	185	925,000	50	925,000	50	1,850,000	185	925,000	50	925,000	50

185

190

Glu	Pro	Val	Ala	Pro	Arg	Glu	Asp	Glu	Gln	Ala	Pro	Thr	Ala	Pro	Val
		195					200					205			
Glu	Pro	Glu	Lys	Gln	Pro	Glu	Val	Pro	Glu	Glu	Glu	Lys	Ala	Val	Glu
	210					215					220				
Glu	Thr	Pro	Lys	Pro	Glu	Asp	Lys	Ile	Lys	Gly	Ile	Gly	Thr	Lys	Glu
225					230					235					240
Pro	Val	Asp	Lys	Ser	Glu	Leu	Asn	Asn	Gln	Ile	Asp	Lys	Ala	Ser	Ser
				245					250					255	
Val	Ser	Pro	Thr	Asp	Tyr	Ser	Thr	Ala	Ser	Tyr	Asn	Ala	Leu	Gly	Pro
			260					265					270		
Val	Leu	Glu	Thr	Ala	Lys	Gly	Val	Tyr	Ala	Ser	Glu	Pro	Val	Lys	Gln
		275					280					285			
Pro	Glu	Val	Asn	Ser	Glu	Thr	Asn	Lys	Leu	Lys	Thr	Ala	Ile	Asp	Ala
	290					295					300				
Leu	Asn	Val	Asp	Lys	Thr	Glu	Leu	Asn	Asn	Thr	Ile	Ala	Asp	Ala	Lys
305					310					315					320
Thr	Lys	Val	Lys	Glu	His	Tyr	Ser	Asp	Arg	Ser	Trp	Gln	Asn	Leu	Gln
				325					330					335	
Thr	Glu	Val	Thr	Lys	Ala	Glu	Lys	Val	Ala	Ala	Asn	Thr	Asp	Ala	Lys
			340					345					350		
Gln	Ser	Glu	Val	Asn	Glu	Ala	Val	Glu	Lys	Leu	Thr	Ala	Thr	Ile	Glu
		355					360					365			
Lys	Leu	Val	Glu	Leu	Ser	Glu	Lys	Pro	Ile	Leu	Thr	Leu	Thr	Ser	Thr
	370					375					380				
Asp	Lys	Lys	Ile	Leu	Glu	Arg	Glu	Ala	Val	Ala	Lys	Tyr	Thr	Leu	Glu
385					390					395					400
Asn	Gln	Asn	Lys	Thr	Lys	Ile	Lys	Ser	Ile	Thr	Ala	Glu	Leu	Lys	Lys
				405					410					415	
Gly	Glu	Glu	Val	Ile	Asn	Thr	Val	Val	Leu	Thr	Asp	Asp	Lys	Val	Thr
			420					425					430		
Thr	Glu	Thr	Ile	Ser	Ala	Ala	Phe	Lys	Asn	Leu	Glu	Tyr	Tyr	Lys	Glu
		435					440					445			
Tyr	Thr	Leu	Ser	Thr	Thr	Met	Ile	Tyr	Asp	Arg	Gly	Asn	Gly	Glu	Glu
	450					455					460				
Thr	Glu	Thr	Leu	Glu	Asn	Gln	Asn	Ile	Gln	Leu	Asp	Leu	Lys	Lys	Val
465					470					475					480
Glu	Leu	Lys	Asn	Ile	Lys	Arg	Thr	Asp	Leu	Ile	Lys	Tyr	Glu	Asn	Gly
				485					490					495	
Lys	Glu	Thr	Asn	Glu	Ser	Leu	Ile	Thr	Thr	Ile	Pro	Asp	Asp	Lys	Ser
			500					505					510		
Asn	Tyr	Tyr	Leu	Lys	Ile	Thr	Ser	Asn	Asn	Gln	Lys	Thr	Thr	Leu	Leu

515

520

525

Ala Val Lys Asn Ile Glu Glu Thr Thr Val Asn Gly Thr Pro Val Tyr
 530 535 540

Lys Val Thr Ala Ile Ala Asp Asn Leu Val Ser Arg Thr Ala Asp Asn
 545 550 555 560

Lys Phe Glu Glu Glu
 565

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA	60
TAAATTTGAA GAAGAATACG TTCACTATAT TGAAAAACCT AAAGTCCACG AAGATAATGT	120
ATATTATAAT TTCAAAGAAT TAGTGGAAGC TATTCAAAAC GATCCTTCAA AAGAATATCG	180
TCTGGGACAA TCAATGAGCG CTAGAAATGT TGTTCCTAAT GGAAAATCAT ATATCACTAA	240
AGAATTCACA GGAAAACCTT TAAGTTCTGA AGGAAAACAA TTTGCTATTA CTGAATTGGA	300
ACATCCATTA TTTAATGTGA TAACAAACGC AACGATAAAT AATGTGAATT TTGAAAATGT	360
AGAGATAGAA CGTTCTGGTC AAGATAATAT TGCATCATTA GCCAATACTA TGAAAGGTTT	420
TTCAGTTATT ACAAATGTCA AAATTACAGG CACACTTTCA GGTCGTAATA ATGTTGCTGG	480
ATTTGTAAAT AATATGAATG ATGGAACGCG TATTGAAAAT GTTGCTTTCT TTGGCAAACT	540
ACACTCTACA AGTGGAATG GCTCTCATAC AGGGGGAATT GCAGGTACAA ACTATAGAGG	600
AATTGTTAGA AAAGCATATG TTGATGCTAC TATTACAGGA AACAAAACAC GCGCCAGCTT	660
GTTAGTTCCT AAAGTAGATT ATGGATTAAC TCTAGACCAT CTTATTGGTA CAAAAGCTCT	720
CCTAACTGAG TCGGTTGTAA AAGGTAAAT AGATGTTTCA AATCCAGTAG AAGTTGGAGC	780
AATAGCAAGT AAGACTTGGC CTGTAGGTAC GGTAAGTAAT TCTGTCAGCT ATGCTAAGAT	840
TATCCGTGGA GAGGAGTTAT TCGGCTCTAA CGACGTTGAT GATTCTGATT ATGCTAGTGC	900
TCATATAAAA GATTTATATG CGGTAGAGGG ATATTCGTCA GGTAATAGAT CATTTAGGAA	960
ATCTAAAACA TTTACTAAAT TAACTAAAGA ACAAGCTGAT GCTAAAGTTA CTACTTTCAA	1020
TATTACTGCT GATAAATTAG AAAGTGATCT ATCTCCTCTT GCAAACTTA ATGAAGAAAA	1080
AGCCTATTCT AGTATTCAAG ATTATAACGC TGAATATAAC CAAGCCTATA AAAATCTTGA	1140
AAAATTAATA CCATTCTACA ATAAAGATTA TATTGTATAT CAAGGTAATA AATTAAATAA	1200

AGAACACCAT CTAAATACTA AAGAAGTTCT TTCTGTTACC GCGATGAACA ACAATGAGTT 1260
TATCACAAAC CTAGATGAAG CTAATAAAAT TATTGTTTAC TATGCGGACG GTACAAAAGA 1320
TTACTTTAAC TTGTCTTCTA GCAGTGAAGG TTTAAGTAAT GTAAAAGAAT ATACTATAAC 1380
TGACTTAGGA ATTAAATATA CACCTAATAT CGTTCAAAAA GATAACACTA CTCTTGTTAA 1440
TGATATAAAA TCTATTTTAT AATCAGTAGA GCTTCAGTCT CAAACGATGT ATCAGCATCT 1500
AAATCGATTA GGTGACTATA GAGTTAATGC AATCAAAGAT TTATATTTAG AAGAAAGCTT 1560
CACAGATGTT AAAGAAAACT TAACAAACCT AATCACAAAA TTAGTTCAAA ACGAAGAACA 1620
TCAACTAAAT GATTCTCCAG CTGCTCGTCA AATGATTCGT GATAAAGTCG AGAAAAACAA 1680
AGCAGCTTTA TTACTAGGTT TAACCTACCT AAATCGTTAC TATGGAGTTA AATTTGGTGA 1740
TGTTAATATT AAAGAATTAA TGCTATTCAA ACCAGATTTC TATGGTGAAA AAGTTAGCGT 1800
ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT 1860
CGACGCATTC GGTCAAGTA 1879

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Thr	Pro	Val	Tyr	Lys	Val	Thr	Ala	Ile	Ala	Asp	Asn	Leu	Val	Ser	Arg
1				5					10					15	
Thr	Ala	Asp	Asn	Lys	Phe	Glu	Glu	Glu	Tyr	Val	His	Tyr	Ile	Glu	Lys
			20					25					30		
Pro	Lys	Val	His	Glu	Asp	Asn	Val	Tyr	Tyr	Asn	Phe	Lys	Glu	Leu	Val
		35					40					45			
Glu	Ala	Ile	Gln	Asn	Asp	Pro	Ser	Lys	Glu	Tyr	Arg	Leu	Gly	Gln	Ser
	50				55						60				
Met	Ser	Ala	Arg	Asn	Val	Val	Pro	Asn	Gly	Lys	Ser	Tyr	Ile	Thr	Lys
65				70					75					80	
Glu	Phe	Thr	Gly	Lys	Leu	Leu	Ser	Ser	Glu	Gly	Lys	Gln	Phe	Ala	Ile
			85						90					95	
Thr	Glu	Leu	Glu	His	Pro	Leu	Phe	Asn	Val	Ile	Thr	Asn	Ala	Thr	Ile
			100						105					110	
Asn	Asn	Val	Asn	Phe	Glu	Asn	Val	Glu	Ile	Glu	Arg	Ser	Gly	Gln	Asp
		115					120					125			
Asn	Ile	Ala	Ser	Leu	Ala	Asn	Thr	Met	Lys	Gly	Ser	Ser	Val	Ile	Thr
	130					135					140				

Asn 145	Val	Lys	Ile	Thr	Gly 150	Thr	Leu	Ser	Gly	Arg 155	Asn	Asn	Val	Ala	Gly 160
Phe	Val	Asn	Asn	Met 165	Asn	Asp	Gly	Thr	Arg 170	Ile	Glu	Asn	Val	Ala 175	Phe
Phe	Gly	Lys	Leu 180	His	Ser	Thr	Ser	Gly 185	Asn	Gly	Ser	His	Thr 190	Gly	Gly
Ile	Ala	Gly 195	Thr	Asn	Tyr	Arg	Gly 200	Ile	Val	Arg	Lys	Ala 205	Tyr	Val	Asp
Ala	Thr 210	Ile	Thr	Gly	Asn	Lys 215	Thr	Arg	Ala	Ser	Leu 220	Leu	Val	Pro	Lys
Val 225	Asp	Tyr	Gly	Leu 230	Thr	Leu	Asp	His	Leu	Ile 235	Gly	Thr	Lys	Ala	Leu 240
Leu	Thr	Glu	Ser 245	Val	Val	Lys	Gly	Lys	Ile 250	Asp	Val	Ser	Asn	Pro 255	Val
Glu	Val	Gly 260	Ala	Ile	Ala	Ser	Lys	Thr 265	Trp	Pro	Val	Gly	Thr 270	Val	Ser
Asn	Ser	Val 275	Ser	Tyr	Ala	Lys	Ile 280	Ile	Arg	Gly	Glu	Glu 285	Leu	Phe	Gly
Ser 290	Asn	Asp	Val	Asp	Asp 295	Ser	Asp	Tyr	Ala	Ser	Ala 300	His	Ile	Lys	Asp
Leu 305	Tyr	Ala	Val	Glu	Gly 310	Tyr	Ser	Ser	Gly	Asn 315	Arg	Ser	Phe	Arg	Lys 320
Ser	Lys	Thr	Phe 325	Thr	Lys	Leu	Thr	Lys	Glu 330	Gln	Ala	Asp	Ala 335	Lys	Val
Thr	Thr	Phe 340	Asn	Ile	Thr	Ala	Asp	Lys 345	Leu	Glu	Ser	Asp	Leu 350	Ser	Pro
Leu	Ala 355	Lys	Leu	Asn	Glu	Glu	Lys 360	Ala	Tyr	Ser	Ser	Ile 365	Gln	Asp	Tyr
Asn 370	Ala	Glu	Tyr	Asn	Gln	Ala 375	Tyr	Lys	Asn	Leu	Glu 380	Lys	Leu	Ile	Pro
Phe 385	Tyr	Asn	Lys	Asp	Tyr 390	Ile	Val	Tyr	Gln	Gly 395	Asn	Lys	Leu	Asn	Lys 400
Glu	His	His	Leu 405	Asn	Thr	Lys	Glu	Val	Leu 410	Ser	Val	Thr	Ala 415	Met	Asn
Asn	Asn	Glu	Phe 420	Ile	Thr	Asn	Leu	Asp 425	Glu	Ala	Asn	Lys	Ile 430	Ile	Val
His	Tyr 435	Ala	Asp	Gly	Thr	Lys	Asp 440	Tyr	Phe	Asn	Leu	Ser 445	Ser	Ser	Ser
Glu 450	Gly	Leu	Ser	Asn	Val	Lys 455	Glu	Tyr	Thr	Ile	Thr 460	Asp	Leu	Gly	Ile
Lys 465	Tyr	Thr	Pro	Asn 470	Ile	Val	Gln	Lys	Asp 475	Asn	Thr	Thr	Leu	Val	Asn 480

Asp Ile Lys Ser Ile Leu Glu Ser Val Glu Leu Gln Ser Gln Thr Met
 485 490 495
 Tyr Gln His Leu Asn Arg Leu Gly Asp Tyr Arg Val Asn Ala Ile Lys
 500 505 510
 Asp Leu Tyr Leu Glu Glu Ser Phe Thr Asp Val Lys Glu Asn Leu Thr
 515 520 525
 Asn Leu Ile Thr Lys Leu Val Gln Asn Glu Glu His Gln Leu Asn Asp
 530 535 540
 Ser Pro Ala Ala Arg Gln Met Ile Arg Asp Lys Val Glu Lys Asn Lys
 545 550 555 560
 Ala Ala Leu Leu Leu Gly Leu Thr Tyr Leu Asn Arg Tyr Tyr Gly Val
 565 570 575
 Lys Phe Gly Asp Val Asn Ile Lys Glu Leu Met Leu Phe Lys Pro Asp
 580 585 590
 Phe Tyr Gly Glu Lys Val Ser Val Leu Asp Arg Leu Ile Glu Ile Gly
 595 600 605
 Ser Lys Glu Asn Asn Ile Lys Gly Ser Arg Thr Phe Asp Ala Phe Gly
 610 615 620
 Gln Val
 625

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT	60
CGACGCATTC GGTCAGTAT TGGCTAAATA TACTAAATCA GGTAATTTAG ATGCATTTTT	120
AAATTATAAT AGACAATTGT TCACAAATAT AGACAATATG AACGATTGGT TTATTGATGC	180
TACAGAAGAC CATGTCTACA TCGCAGAACG CGCTTCTGAG GTCGAAGAAA TTAAAAATTC	240
TAAACATCGT GCATTCGATA ATTTAAAACG AAGTCACCTT AGAAATACTA TACTCCCACT	300
ACTGAATATT GATAAAGCAC ATCTTTATTT AATTTCAAAT TATAATGCAA TTGCCTTTGG	360
TAGTGCAGAG CGATTAGGTA AAAAATCATT AGAAGATATT AAAGATATCG TTAACAAAGC	420
TGCAGATGGT TATAGAACT ATTATGATTT CTGGTATCGT CTAGCGTCTG ATAACGTAA	480
ACAACGACTA CTAAGAGATG CTGTTATTCC TATTTGGGAA GGTATAACG CTCCTGGTGG	540
ATGGGTTGAA AAATATGGCC GCTATAATAC CGACAAAGTA TATACTCCTC TTAGAGAATT	600

CTTTGGTCCT ATGGATAAGT ATTATAATTA TAATGGAACA GGAGCTTATG CTGCTATATA 660
 TCCTAACTCT GATGATATTA GAACTGATGT AAAATATGTT CATTTAGAAA TGGTTGGTGA 720
 ATACGGTATT TCAGTTTACA CACATGAAAC AACACACGTC AACGACCGTG CGATTTACTT 780
 AGGTGGCTTT GGACACCGTG AAGGTACTGA TGCTGAAGCA TATGCTCAGG GTATGCTACA 840
 AACTCCTGTT ACTGGTAGTG GATTTGATGA GTTTGGTTCT TTAGGTATTA ATATGGTATT 900
 TAAACGCAAA AATGATGGGA ATCAGTGGTA TATTACAGAT CCAAAAAGCTC TAAAAACACG 960
 AGAAGATATT AATAGATATA TGAAGGGTTA TAATGACACT TTAAGTCTTC TTGATGAAAT 1020
 TGAGGCTGAA TCTGTGATTT CTCAACAAAA TAAAGATTTA AATAGTGCAT GGTTCAAAAA 1080
 AATAGATAGA GAATACCGTG ATAACAATAA ATTAAATCAA TGGGATAAAA TTCGAAATCT 1140
 AAGTCAAGAA GAGAAAAATG AATTAAATAT TCAATCTGTT AATGATTTAG TTGATCAACA 1200
 ATTAATGACT AATCGCAATC CAGGTAATGG TATCTATAAA CCCGAAGCAA TTAGCTATAA 1260
 CGATCAATCA CCTTATGTAG GTGTTAGAAT GATGACCGGT ATCTACGGAG GTAATACTAG 1320
 TAAAGGTGCT CCTGGAGCTG TTTCATTCAA ACATAATGCT TTTAGATTAT GGGGTTACTA 1380
 CGGATACGAA AATGGGTTCT TAGGTTATGC TTCAAATAAA TATAACAAC AATCTAAAC 1440
 AGATGGTGAG TCTGTTCTAA GTGATGAATA TATTATCAAG AAAATATCTA ACAATACATT 1500
 TAATACTATT GAAGAATTTA AAAAAGCTTA CTTCAAAGAA GTTAAAGATA AAGCAACGAA 1560
 AGGATTAACA ACATTCTGAAG TAAATGGTTC TTCCGTTTCA TCATACGATG ATTTACTGAC 1620
 ATTGTTTAAA GAAGCTGTTA AAAAAGATGC CGAACTCTT AAACAAGAAG CAAACGGTAA 1680
 TAAAACAGTA TCTATGAATA ATACAGTTAA ATTAAAAGAA GCTGTTTATA AGAACTTCT 1740
 TCAACAAACA AATAGCTTTA AAAGTTCAAT CTTTAAA 1777

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Leu Asp Arg Leu Ile Glu Ile Gly Ser Lys Glu Asn Asn Ile Lys Gly
 1 5 10 15

Ser Arg Thr Phe Asp Ala Phe Gly Gln Val Leu Ala Lys Tyr Thr Lys
 20 25 30

Ser Gly Asn Leu Asp Ala Phe Leu Asn Tyr Asn Arg Gln Leu Phe Thr
 35 40 45

Asn Ile Asp Asn Met Asn Asp Trp Phe Ile Asp Ala Thr Glu Asp His

50					55					60						
Val	Tyr	Ile	Ala	Glu	Arg	Ala	Ser	Glu	Val	Glu	Glu	Ile	Lys	Asn	Ser	
65					70					75					80	
Lys	His	Arg	Ala	Phe	Asp	Asn	Leu	Lys	Arg	Ser	His	Leu	Arg	Asn	Thr	
				85					90					95		
Ile	Leu	Pro	Leu	Leu	Asn	Ile	Asp	Lys	Ala	His	Leu	Tyr	Leu	Ile	Ser	
			100					105					110			
Asn	Tyr	Asn	Ala	Ile	Ala	Phe	Gly	Ser	Ala	Glu	Arg	Leu	Gly	Lys	Lys	
		115					120					125				
Ser	Leu	Glu	Asp	Ile	Lys	Asp	Ile	Val	Asn	Lys	Ala	Ala	Asp	Gly	Tyr	
	130					135					140					
Arg	Asn	Tyr	Tyr	Asp	Phe	Trp	Tyr	Arg	Leu	Ala	Ser	Asp	Asn	Val	Lys	
145					150					155					160	
Gln	Arg	Leu	Leu	Arg	Asp	Ala	Val	Ile	Pro	Ile	Trp	Glu	Gly	Tyr	Asn	
				165					170					175		
Ala	Pro	Gly	Gly	Trp	Val	Glu	Lys	Tyr	Gly	Arg	Tyr	Asn	Thr	Asp	Lys	
			180					185					190			
Val	Tyr	Thr	Pro	Leu	Arg	Glu	Phe	Phe	Gly	Pro	Met	Asp	Lys	Tyr	Tyr	
		195					200					205				
Asn	Tyr	Asn	Gly	Thr	Gly	Ala	Tyr	Ala	Ala	Ile	Tyr	Pro	Asn	Ser	Asp	
	210					215					220					
Asp	Ile	Arg	Thr	Asp	Val	Lys	Tyr	Val	His	Leu	Glu	Met	Val	Gly	Glu	
225					230					235					240	
Tyr	Gly	Ile	Ser	Val	Tyr	Thr	His	Glu	Thr	Thr	His	Val	Asn	Asp	Arg	
				245					250					255		
Ala	Ile	Tyr	Leu	Gly	Gly	Phe	Gly	His	Arg	Glu	Gly	Thr	Asp	Ala	Glu	
			260					265					270			
Ala	Tyr	Ala	Gln	Gly	Met	Leu	Gln	Thr	Pro	Val	Thr	Gly	Ser	Gly	Phe	
		275					280					285				
Asp	Glu	Phe	Gly	Ser	Leu	Gly	Ile	Asn	Met	Val	Phe	Lys	Arg	Lys	Asn	
	290					295					300					
Asp	Gly	Asn	Gln	Trp	Tyr	Ile	Thr	Asp	Pro	Lys	Thr	Leu	Lys	Thr	Arg	
305					310					315					320	
Glu	Asp	Ile	Asn	Arg	Tyr	Met	Lys	Gly	Tyr	Asn	Asp	Thr	Leu	Thr	Leu	
				325					330					335		
Leu	Asp	Glu	Ile	Glu	Ala	Glu	Ser	Val	Ile	Ser	Gln	Gln	Asn	Lys	Asp	
			340					345					350			
Leu	Asn	Ser	Ala	Trp	Phe	Lys	Lys	Ile	Asp	Arg	Glu	Tyr	Arg	Asp	Asn	
		355					360					365				
Asn	Lys	Leu	Asn	Gln	Trp	Asp	Lys	Ile	Arg	Asn	Leu	Ser	Gln	Glu	Glu	
	370					375					380					
Lys	Asn	Glu	Leu	Asn	Ile	Gln	Ser	Val	Asn	Asp	Leu	Val	Asp	Gln	Gln	

385 390 395 400

Leu Met Thr Asn Arg Asn Pro Gly Asn Gly Ile Tyr Lys Pro Glu Ala
 405 410 415

Ile Ser Tyr Asn Asp Gln Ser Pro Tyr Val Gly Val Arg Met Met Thr
 420 425 430

Gly Ile Tyr Gly Gly Asn Thr Ser Lys Gly Ala Pro Gly Ala Val Ser
 435 440 445

Phe Lys His Asn Ala Phe Arg Leu Trp Gly Tyr Tyr Gly Tyr Glu Asn
 450 455 460

Gly Phe Leu Gly Tyr Ala Ser Asn Lys Tyr Lys Gln Gln Ser Lys Thr
465 470 475 480

Asp Gly Glu Ser Val Leu Ser Asp Glu Tyr Ile Ile Lys Lys Ile Ser
 485 490 495

Asn Asn Thr Phe Asn Thr Ile Glu Glu Phe Lys Lys Ala Tyr Phe Lys
 500 505 510

Glu Val Lys Asp Lys Ala Thr Lys Gly Leu Thr Thr Phe Glu Val Asn
 515 520 525

Gly Ser Ser Val Ser Ser Tyr Asp Asp Leu Leu Thr Leu Phe Lys Glu
 530 535 540

Ala Val Lys Lys Asp Ala Glu Thr Leu Lys Gln Glu Ala Asn Gly Asn
545 550 555 560

Lys Thr Val Ser Met Asn Asn Thr Val Lys Leu Lys Glu Ala Val Tyr
 565 570 575

Lys Lys Leu Leu Gln Gln Thr Asn Ser Phe Lys Thr Ser Ile Phe Lys
 580 585 590

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

TAAGACAGAT GAACGGAGCA AGGTGTTTGA CTTTTCATT CCCTACTATA CTGCAAAAAA	60
TAAACTCATT GTCAAAAAAT CTGACTTGAC TACTTATCAG TCTGTAAACG ACTTGGCGCA	120
GAAAAAGGTT GGAGCGCAGA AAGGTTTCGAT TCAAGAGACG ATGGCGAAAG ATTTGCTACA	180
AAATTCTTCC CTCGTATCTC TGCCTAAAAA TGGGAATTTA ATCACAGATT TAAAATCAGG	240
ACAAGTGGAT GCCGTTATCT TTGAAGAACC TGTTTCCAAG GGATTTGTGG AAAATAATCC	300
TGATTTAGCA ATCGCAGACC TCAATTTTGA AAAAGAGCAA GATGATTCCT ACGCGGTAGC	360
CATgAAAAAA GATAGCAAGA AATTGAAGAG GCAGTTCGAT AAAACCATTC AAAAGTTGAA	420

GGAGTCTGGG GAATTAGACA AACTCATTGA GGAAGCCTTA

460

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Lys Thr Asp Glu Arg Ser Lys Val Phe Asp Phe Ser Ile Pro Tyr Tyr
1           5           10           15

Thr Ala Lys Asn Lys Leu Ile Val Lys Lys Ser Asp Leu Thr Thr Tyr
          20           25           30

Gln Ser Val Asn Asp Leu Ala Gln Lys Lys Val Gly Ala Gln Lys Gly
          35           40           45

Ser Ile Gln Glu Thr Met Ala Lys Asp Leu Leu Gln Asn Ser Ser Leu
50           55           60

Val Ser Leu Pro Lys Asn Gly Asn Leu Ile Thr Asp Leu Lys Ser Gly
65           70           75           80

Gln Val Asp Ala Val Ile Phe Glu Glu Pro Val Ser Lys Gly Phe Val
          85           90           95

Glu Asn Asn Pro Asp Leu Ala Ile Ala Asp Leu Asn Phe Glu Lys Glu
          100          105          110

Gln Asp Asp Ser Tyr Ala Val Ala Met Lys Lys Asp Ser Lys Lys Leu
          115          120          125

Lys Arg Gln Phe Asp Lys Thr Ile Gln Lys Leu Lys Glu Ser Gly Glu
130          135          140

Leu Asp Lys Leu Ile Glu Glu Ala Leu
145          150

```

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```

CTGTGAGAAT CAAGCTACAC CCAAGAGAC TAGCGCTCAA AAGACAATCG TCCTTGCTAC      60
AGCTGGCGAC GTGCCACCAT TTGACTACGA AGACAAGGGC AATCTGACAG GCTTTGATAT      120
CGAAGTTTTA AAGGCAGTAG ATGAAAACT CAGCGACTAC GAGATTCAAT TCCAAAGAAC      180

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CGCCTGGGAG AGCATCTTCC CAGGACTTGA TTCTGGTCAC TATCAGGCTG CGGCCAATAA 240
 CTTGAGTTAC ACAAAGAGC GTGCTGAAAA ATACCTTTAC TCGCTTCCAA TTTCCAACAA 300
 TCCCCTCGTC CTTGTCAGCA ACAAGAAAAA TCCTTTGACT TCTCTTGACC AGATCGCTGG 360
 TAAAACAACA CAAGAGGATA CCGGAACCTC TAACGCTCAA TTCATCAATA ACTGGAATCA 420
 GAAACACACT GATAATCCCG CTACAATTAA TTTTCTGGT GAGGATATTG GTAAACGAAT 480
 CCTAGACCTT GCTAACGGAG AGTTTGATTT CCTAGTTTTT GACAAGGTAT CCGTTCAAAA 540
 GATTATCAAG GACCGTGGTT TAGACCTCTC AGTCGTTGAT TTACCTTCTG CAGATAGCCC 600
 CAGCAATTAT ATCATTTTCT CAAGCGACCA AAAAGAGTTT AAAGAGCAAT TTGATAAAGC 660
 GCTCAAAGAA CTCTATCAAG ACGGAACCTT TGAAAACTC AGCAATACCT ATCTAGGTGG 720
 TTCTTACCTC CCAGATCAAT CTCAGTTACA A 751

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Cys	Glu	Asn	Gln	Ala	Thr	Pro	Lys	Glu	Thr	Ser	Ala	Gln	Lys	Thr	Ile	1	5	10	15
Val	Leu	Ala	Thr	Ala	Gly	Asp	Val	Pro	Pro	Phe	Asp	Tyr	Glu	Asp	Lys	20	25	30	
Gly	Asn	Leu	Thr	Gly	Phe	Asp	Ile	Glu	Val	Leu	Lys	Ala	Val	Asp	Glu	35	40	45	
Lys	Leu	Ser	Asp	Tyr	Glu	Ile	Gln	Phe	Gln	Arg	Thr	Ala	Trp	Glu	Ser	50	55	60	
Ile	Phe	Pro	Gly	Leu	Asp	Ser	Gly	His	Tyr	Gln	Ala	Ala	Ala	Asn	Asn	65	70	75	80
Leu	Ser	Tyr	Thr	Lys	Glu	Arg	Ala	Glu	Lys	Tyr	Leu	Tyr	Ser	Leu	Pro	85	90	95	
Ile	Ser	Asn	Asn	Pro	Leu	Val	Leu	Val	Ser	Asn	Lys	Lys	Asn	Pro	Leu	100	105	110	
Thr	Ser	Leu	Asp	Gln	Ile	Ala	Gly	Lys	Thr	Thr	Gln	Glu	Asp	Thr	Gly	115	120	125	
Thr	Ser	Asn	Ala	Gln	Phe	Ile	Asn	Asn	Trp	Asn	Gln	Lys	His	Thr	Asp	130	135	140	
Asn	Pro	Ala	Thr	Ile	Asn	Phe	Ser	Gly	Glu	Asp	Ile	Gly	Lys	Arg	Ile	145	150	155	160

Ser Tyr Leu Pro Asp Gln Ser Gln Leu Gln
245 250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

30

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CAGTGTCGAC TAACTCTAGG TCGGAAAC

28

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GACTGGATCC TGAGAATCAA GCTACACCCA AAGAG

35

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGTCAAGCTT TTGTAAGTGA GATTGATCTG G

31

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GACTGGATCC TGGTAACCGC TCTTCTCGTA ACGCAGC

37

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

AGTCAAGCTT TTTCAGGAAC TTTTACGCTT CC

32

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

AGTCAGATCT TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGC

45

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

ACTGAAGCTT TTTTGT TTTT CAAGAATTCA TCG

33

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

GACTGGATCC TGGTCAAGGA ACTGCTTCTA AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

AGTCAAGCTT TCACAAATTC GTTGGTGAAG CC

32

(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

GACTGGATCC TAGCTCAGGT GGAAACGCTG GTTCATCC

38

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

AGTCAAGCTT ATCAACTTTT CCACCTTCAA CAACC

35

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

GTCAAGATCT CTCCAATAT GGTAATCTG CGGATGG

37

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

AGTCCTGCAG ATCCACATCC GCTTTCATCG GGTTAAAGAA GG

42

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

GACTGGATCC TGGGAAAAAT TCTAGCGAAA CTAGTGG

37

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

GTCAGTGCAG CTGTCCTTCT TTTACTTCTT TGGTTGC

37

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

GACTGGATCC TGCTAGCGGA AAAAAAGATA CAACTTCTGG

40

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

CTGAAAGCTT TTTTGCCAAT CCTTCAGCAA TCTTGTC

37

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

GACTAGATCT TGGCTCAAAA AATACAGCTT CAAGTCC

37

(2) INFORMATION FOR SEQ ID NO: 248:

2025-11-11 14:53:00

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AGTCCTGCAG GTTTTTGTTT GCTTGGTATT GGTCTG

35

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

GACTGGATCC TAGTACAAAC TCAAGCACTA GTCAGACAGA G

41

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CAGTCTGCAG TTTCAAAGCT TTTTGTATGT CTTC

34

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

GACTGGATCC TGGCAATTCT GCGGAAGTA AAGATGC

37

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

36

(2) INFORMATION FOR SEQ ID NO: 253:

(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(2) INFORMATION FOR SEQ ID NO: 254:

(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

31

(2) INFORMATION FOR SEQ ID NO: 255:

(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

38

(2) INFORMATION FOR SEQ ID NO: 256:

(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

37

AGTCAAGCTT AGAGTTAACA TGGTGCTTGC CAATAGG

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GACTGGATCC AACTCAGAA AAGAAAGCAG ACAATGC

37

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCAAGCTT CCAAACTGGT TGATCCAAAC CATCTG

36

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

GACTGGATCC TTCGAAAGGG TCAGAAGGTG CAGACC

36

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGTCAAGCTT CTGTAGGCTT GGTGTGCCCC AGTTGC

36

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

33

33

(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

31

31

(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

29

29

(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

28

28

(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

35

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

CTGAGTCGAC AATATTCTGT AGGAATGCTT CGAATTTG

38

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CTGAGGATCC GACTTTTAAC AATAAACTA TTGAAGAG

38

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GTCACCTGCAG GTTGTCACCT CCAAAAATCA CGG

33

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GACTGGATCC CTTTACAGGT AAACAACACTAC AAGTCGG

37

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CAGTAAGCTT TTCGAAGTTT GGCTCAGAAT TG

32

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GACTGGATCC CCAGGCTGAT ACAAGTATCG CA

32

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CAGTAAGCTT ATCTGCAGTA TGGCTAGATG G

31

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

GACTGGATCC GTCTGTATCA TTTGAAAACA AAGAAAC

37

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CAGTCTGCAG TTTTACTGTT GCTGTGCTTG TG

32

(2) INFORMATION FOR SEQ ID NO: 275:

09551-0100
T229460

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ACTGAGATCT TGGTCAAAAG GAAAGTCAGA CAGGAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGTAAGCTT ATTCCTGAGC TTTTGTGATA AAGGTTGCGC A

41

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

ACTGGGATCC GAAGGATAGA TATATTTTAG CATTTGAGAC

40

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AGTCAAGCTT CCATGGTATC AAAGGCAAGA CTTGG

35

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

34

34

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

36

36

(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

37

37

(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

40

(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

37

37

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

TCAGCTCGAG TTCTTTGACA TCTCCATCAT AAGTCGC

37

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

GACTGGATCC GGTTTTGAGA AAGTATTTGC AGGGG

35

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

CAGTAAGCTT GGATTTTTTC ATGGATGCAA TTTTTTTGG

39

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GACTGGATCC GACAACATTT ACTATCCATA CAGTAGAGTC AGC

43

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

40

(D) TOPOLOGY: linear

30

30

(D) TOPOLOGY: linear

37

37

(D) TOPOLOGY: linear

36

36

(D) TOPOLOGY: linear

35

35

(2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

GACTGGATCC TTATAAGGGT GAATTAGAAA AAGG

34

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GACTAAGCTT CTTATTAGGA TTGTTAGTAG TTG

33

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

GACTGGATCC GAATGTTTCAG GCTCAAGAAA GTTCAGG

37

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GACTAAGCTT TTCCCCTGAT GGAGCAAAGT AATACC

36

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

GACTGGATCC CTTGGGTGTA ACCCATATCC AGCTCCTTCC

40

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GACTGTCGAC TTCAGCTTGT TTATCTGGGG TTGC

34

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GACTGGATCC TAGTGATGGT ACTTGGCAAG GAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

ACTGCTGCAG ATCTTTGCCA CCTAGCTTCT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

GTCAGGATCC TGGGATTCAA TATGTCAGAG ATGATACTAG

40

(2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

CTAGAAGCTT ACGCACCCAT TCACCATTAT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GTCAGGATCC GGATAATAGA GAAGCATTA AAACC

35

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGTCAAGCTT GACAAAATCT TGAAACTCCT CTGGTC

36

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GTCAGGATCC AGATTTTGTC GAGGAGTGTC ATACC

35

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

AGTCAAGCTT TCCCTTTTTA CCCTTACGAA TCCAGG

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC ATCTGTAGTT TATGCGGATG AAACACTTAT TAC

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGTCGAC GCTTTGGTAG AGATAGAAGT CATG

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC TTACTTTGGT ATCGTAGATA CAGCCGGC

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AGTCAAGCTT TGTTAATTGC GTACCTTCTA AGCGACC

37

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GACTGGATCC AGCTAAGGTT GCATGGGATG CGATTCC

37

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GACTGTCGAC CTGGGCTTTA TTAGTTTGAC TAGC

34

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

CAGTGGATCC CTATCACTAT GTAAATAAAG AGA

33

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

ACTGAAGCTT TTCTGTCCCT GTTTGAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

CAGTGGATCC TGAGACTCCT CAATCAATAA CAAA

34

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

ACGTAAGCTT ATAATCAGTA GGAGAACTG AACT

34

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CAGTGGATCC GGATGCTCAA GAACTGCGG

30

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

GACTAAGCTT TTGCCTCTCA TTCTTGCTTC C

31

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

CAGTGGATCC CGACAAAGGT GAGACTGAG

29

(2) INFORMATION FOR SEQ ID NO: 320:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

ACGTAAGCTT ATTTCTTAAT TCAAGTGTTT TCTCTG

36

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GACTGGATCC AAATCAATTG GTAGCACAAG ATCC

34

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CAGTGTGAC ATTAGGAGCC ACTGGTCTC

29

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

CAGTGGATCC CAAACAGTCA GCTTCAGGAA C

31

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

GACTCTGCAG TTTAATCTTG TCCCAGGTGG 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC ATTCGATGAT GCGGATGAAA AG 32

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTAAGCTT CATTGTCTT TGGGTATTTC GCA 33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAGTGGATCC GGAGAGTCGA TCAAAAGTAG 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTCACTGCAG TTGCTCGTCT CGAGGTTC 28

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

CAGTGGATCC ATGGACAACA GGAAACTGGG AC

32

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

CAGTAAGCTT ATTAGCTTCT GTACCTGTGT TTG

33

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

GACTGGATCC CGATGGGCTC AATCCAACCC CAGGTCAAGT C

41

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GACTCTGCAG CATAGCTTTA TCCTCTGACA TCATCGTATC

40

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GACTGGATCC TTCCAATCAA AAACAGGCAG ATGG

34

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

GACTAAGCTT GAGTCCCATATA GTCCAAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

AGTCGGATCC TATCACAGGA TCGAACGGTA AGACAACC

38

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

ACTGGTCGAC TTCTTTTAAC TCCGCTACTG TGTC

34

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CAGTGGATCC AAGTTCATCG AAGATGGTTG GGAAGTCC

38

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GATCGTCGAC CCGCTCCCAC ATGCTCAACC TT

32

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

TGACGGATCC ATCGCTAGCT AGTGAAATGC AAGAAAG

37

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

TGACAAGCTT ATTCGTTTTT GAACTAGTTG CTTTCGT

37

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GACTGGATCC GCACCAGATG GGGCACAAGG TTCAGGG

37

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TGACAAGCTT AACTTGTAAC GAACAGTTCA ATCTG

35

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GACTAGATCT TTTTAACCCA ACTGTTGGTA CTTTCC

36

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TGACAAGCTT GTTAGGTGTT ACATTTTGAC CGTC

34

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

ACTGAGATCT TTTTAACCCA ACTGTTGGTA CTTTC

35

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

GACTAAGCTT TCTACGATAA CGATCATTTT CTTTACC

37

(2) INFORMATION FOR SEQ ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GACTGTCGAC TCGTAGATAT TTAAGTCTAA GTGAAGCG

38

(2) INFORMATION FOR SEQ ID NO: 348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AGTCAAGCTT GTTAGGTGTT ACATTTTGCA AGTC

34

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GACTGGATCC CTTTGGTTTT GAAGGAAGTA AG

32

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TGACCTGCAG ACGATTTTGT AAAAATGGAG GTGTATC

37

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CAGTGGATCC CTACTACCTC TCGAGAGAAA G

31

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

ACTGAAGCTT TTCGCTTTTT ACTCGTTTGA CA

32

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CAGTGGATCC TAAGGTCAAA AGTCAGACCG CTAAGAAAGT GC

42

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

CAGTAAGCTT TAGGGTATCC AAATACTGGT TGTGTATG

38

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TGACAGATCT TGACGGGTCT CAGGATCAGA CTCAGG

36

(2) INFORMATION FOR SEQ ID NO: 356:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

TGACAAGCTT CAAAGACATC CACCTCTTGA CCTTTG

36

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

GACTGGATCC TAGAGGCTTT GCCAAATGGT GGGAAGGG

38

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GTCAGTCGAC TTGTTGTAAC ACTTTTCGAG GTTTGGTACC

40

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CAGTGGATCC TCAAAAAGAG AAGGAAACT TGG

33

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

CAGTCTGCAG TTTCTTCAAC AAACCTTGTT CTTG

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CAGTGGATCC ACGTTCTATT GAGGACCACT T

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAGTAAGCTT TTCCTTCTCA GTCAATTCTT TTCC

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC CGCTCAAAAT ACCAGAGGTG TTCAG

(2) INFORMATION FOR SEO ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTAAGCTT AGTACCATGG GTGTGACAGG TTTGAA

(2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

CTGAGGATCC AATTGTACAA TTAGAAAAAG ATAGC

35

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

TGACAAGCTT GCGTTGACTA GGTTC TGCAA TGCC

34

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GACTGGATCC TCTGACCAAG CAAAAAGAAG CAGTCAATGA

40

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

TCAGCAGCTG ATCATTGACT TTACGATTG CTCC

34

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

GACTGGATCC GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC G

41

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAGAAGCTT ATTTTTTGTT TCCTTAATGC GTT

33

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

GACTGGATCC GGGACAAATT CAAAAAATA GGCAAGAGG

39

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

GTCAAAGCTT TGGCTCTTTG ATTGCCAACA ACTG

34

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GACTGGATCC TCGTACCAG CAACAAAGCG AGCAAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

GACTAAGCTT ACTTTTTTCT TTTTCCACAC GA

32

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

CAGTGGATCC GAACCGACAA GTCGCCCACT ATCAAGACT

39

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CTGAAAGCTT TGAATTCTCT TTCTTTTCAG GCT

33

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

TCGAGGATCC GGTGTGTCGGC TGGCAATATA TCCCGT

36

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double -----
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CAGTAAGCTT CCGAACCCAT TCGCCATTAT AGTTGAC

37

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

AGTCGGATCC GGCCAAATCA GAATGGGTAG AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

TGACCTGCAG CTTCTCATTG ATTTTCATCA TCAC

34

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACTGGATCC ATTTGCAGAT GATTCTGAAG GATGG

35

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

TCAGCTGCAG CTTAACCCAT TCACCATTCT AGTTTAAG

38

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

GACTGGATCC TGTCGCTGCA AATGAACTG AAGTAGC

37

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GACTAAGCTT ATACCAAACG CTGACATCTA CGCG

34

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

AGTCAGATCT TACGTCTCAG CCTACTTTTG TAAGAGC

37

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

GACTAAGCTT AACCCATTCA CCATTGGCAT TGAC

34

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CAGTGGATCC TGGACAGGTG AAAGGTCATG CTACATTTGT G

41

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

GACTAAGCTT CAACCATTTGA GACCTTGCAA CAC

33

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GTCAGGATCC GATTGCTCCT TTGAAGGATT TGAGAGAAAC C

41

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GACTAAGCTT CGATCAAAGA TAAGATAAAT ATATATAAAG T

41

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GACTGGATCC TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGG

47

(2) INFORMATION FOR SEQ ID NO: 392:

102210-423260

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TGACAAGCTT ATCTATCAGC TCATTTAATC GTTTTTG

37

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CTGAGGATCC CAACGTTGAG AATTATTTGC GAATG

35

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

TGACAAGCTT GAGTCTACAA AAGTAATGTA C

31

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

GTCAGGATCC CTACTATCAA TCAAGTTCTT CAGCC

35

(2) INFORMATION FOR SEQ ID NO: 396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

TGACAAGCTT GACTGAGGCT TGGACCAGAT TGAAAAG

37

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

GACTGGATCC GACAAAAACA TAAAACGTC CTGAGG

36

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

GACTAAGCTT AGCACGAACT GTGACGCTGG TTCC

34

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

GACTGGATCC TTCTCAGGAG ACCTTTAAAA ATATC

35

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

GACTAAGCTT GTTGGCCATC TTGTACATAC C

31

(2) INFORMATION FOR SEQ ID NO: 401:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

GACTGGATCC AGTAAATGCG CAATCAAATT C

31

(2) INFORMATION FOR SEQ ID NO: 402:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

AGTCCTGCAG GTATTTAGCC CAATAATCTA TAAAGCT

37

(2) INFORMATION FOR SEQ ID NO: 403:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

CAGTGGATCC TTACCGCGTT CATCAAGATG TC

32

(2) INFORMATION FOR SEQ ID NO: 404:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

GACTAAGCTT GCCAGATGTT GAAAAGAGAG TG

32

(2) INFORMATION FOR SEQ ID NO: 405:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

GACTGGATCC GTGGATGGGC TTAACTATC TTCGTATTCG

40

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

AGTCAAGCTT GCTAGTCTTC ACTTTCCTT TCC

33

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

GACTGTCGAC ACTAAACCAG CATCGTTCGC AGGA

34

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

CTGACTGCAG CTTCTTGAAG AAATAATGAT TGTGG

35

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

CAGTGGATCC TGACTACCTT GAAATCCCAC TT

32

(2) INFORMATION FOR SEQ ID NO: 410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

CAGTAAGCTT TTTTAAAGG TTGTAGAATG ATTTCAATC

39

(2) INFORMATION FOR SEQ ID NO: 411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

CAGTGTCGAC TCGTATCTTT TTTTGGAGCA ATGTT

35

(2) INFORMATION FOR SEQ ID NO: 412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

GACTAAGCTT AAATGTTCCG ATACGGGTGA TTG

33

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

CAGTGGATCC GGACTCTCTC AAAGATGTGA AAG

33

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

GACTAAGCTT CTTGAGTTTG TCAAGGATTG CTTT

34

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

CAGTGGATCC CAAGAAATCC TATCATCTCT TCCAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GACTAAGCTT TTCAGAACTA AAAGCCGCAG CTT

33

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

GACTGGATCC ACGAAATGCA GGGCAGACAG

30

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

CAGTAAGCTT ATCAACATAA TCTAGTAAAT AAGCGT

36

(2) INFORMATION FOR SEQ ID NO: 419:

100-423450

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

CAGTGGATCC TGTATAGTTT TTAGCGCTTG TTCTTC

36

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GTCAAAGCTT TGATAGAGTG TCATAATCTT CTTTAG

36

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

GACTGGATCC GTGTGTCGAG CATATTCTGA AG

32

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CAGTAAGCTT ACTTTTACCA TTTCTTTGTT CTGCATC

37

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

GACTGTCGAC GTGTTTGGAT AGCATTCAGA ATCAGACG

38

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

CAGTAAGCTT CGGAAGTAAA GACAATTTTT CC

32

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

CAGTGGATCC GTGCCTAGAT AGTATTATTA CTCAAAC

37

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

GACTAAGCTT TTTGCTTATT TCTCTCAATT TTTC

34

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

CAGTGGATCC CATTAGAAG CAGACCTATC AAAATC

36

(2) INFORMATION FOR SEQ ID NO: 428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

ACTGAAGCTT ATGTAATTTT TTAGATTTT CAATATTTT CAG

43

(2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AGTCGGATCC TAAGGCTGAT AATCGTGTTT AAATG

35

(2) INFORMATION FOR SEQ ID NO: 430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GACTAAGCTT AAAATTAGAT AGACGTTGAG T

31

(2) INFORMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGTCGGATCC CTGTGGCAAT CAGTCAGCTG CTTCC

35

(2) INFORMATION FOR SEQ ID NO: 432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

GACTGTCGAC TTTAATCTTG TCCCAGGTGG TTAATTTGCC

40

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

ACTGGTCGAC TTGTCAACAA CAACATGCTA CTTCTGAG

38

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GACTCTGCAG AAGTTTAACC CACTTATCAT TATCC

35

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACTGGGATCC TTGTTCAAGC AAGTCCGTGA CTAGTGAAC

39

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

GACTAAGCTT GGCTAATTCC TTCAAAGTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 437:

00000-00000

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

AGTCGGATCC CTCGCAAATT GAAAAGGCGG CAGTTAGCC

39

(2) INFORMATION FOR SEQ ID NO: 438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

GACTAAGCTT GTAAATAAGC GTACCTTTTT CTTCC

35

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

TCAGGGATCC TTGTCAGTCA GGTCTAATG GTTCTCAG

38

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

AGTCAAGCTT GGCATTGGCG TCGCCGTCCT TC

32

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

38

GACTGGATCC GGAAACTTCA CAGGATTTTA AAGAGAAG

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

GACTGTCGAC AATCAATCCT TCTTCTGCAC TTCT

34

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

CAGTGGATCC TGTGGTCGAA GTTGAGACTC CTCAATC

37

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GACTAAGCTT TTCTTCAAAT TTATTATCAG C

31

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

AGTCGGATCC AACACCTGTA TATAAAGTTA CAGCAATCG

39

(2) INFORMATION FOR SEQ ID NO: 446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

GACTGTCGAC TACTTGACCG AATGCGTCGA ATGTACG

37

(2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTGAGGATCC ATTAGACAGA TTAATTGAAA TCGG

34

(2) INFORMATION FOR SEQ ID NO: 448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

GACTGTCGAC TTAAAGATT GAAGTTTTAA AGCT

34

(2) INFORMATION FOR SEQ ID NO: 449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TGACGGATCC TAAGACAGAT GAACGGAGCA AGGTG

35

(2) INFORMATION FOR SEQ ID NO: 450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

CTGAAAGCTT TAAGGCTTCC TCAATGAGTT TGTCT

35

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

GACTGGATCC CTGTGAGAAT CAAGCTACAC CCA

33

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

CTGAAAGCTT TTGTAAGTGA GATTGATCTG GGAG

34

450 451 452